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OM nucleic - nucleic search, using sw model

Run on: August 16, 2004, 12:10:55 ; Search time 171 Seconds
(without alignments)
7697.915 Million cell updates/sec

Title: US-10-063-670-5
Perfect score: 2372
Sequence: 1 agcagggaatccgatgtc.....ttaaagcatttagaaaaactt 2372

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PC1US_COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2372	100.0	2372	4	US-09-907-794A-200 Sequence 200, App
2	2372	100.0	2372	4	US-09-905-125A-200 Sequence 200, App
3	2372	100.0	2372	4	US-09-902-775A-200 Sequence 200, App
4	2372	100.0	2404	4	US-09-833-381-849 Sequence 849, App
5	2372	100.0	2404	4	US-09-833-381-853 Sequence 853, App
6	2290.2	96.6	2313	2	US-08-892-880-1 Sequence 1, Appli
7	1994	84.1	2029	4	US-09-232-160-13 Sequence 13, Appl
8	603.6	25.4	1896	4	US-09-724-864-28 Sequence 28, Appl
9	334	14.1	339	2	US-08-892-880-11 Sequence 11, Appl
10	296.8	12.5	492	2	US-08-892-880-12 Sequence 12, Appl
11	239	10.1	241	4	US-09-389-681-324 Sequence 324, App
12	239	10.1	241	4	US-09-620-405B-324 Sequence 324, App
13	239	10.1	241	4	US-09-433-826B-324 Sequence 324, App
14	239	10.1	241	4	US-09-604-287A-324 Sequence 324, App
15	239	10.1	241	4	US-09-834-759-324 Sequence 324, App
16	237	10.0	241	4	US-09-389-681-323 Sequence 323, App
17	237	10.0	241	4	US-09-620-405B-323 Sequence 323, App
18	237	10.0	241	4	US-09-433-826B-323 Sequence 323, App
19	237	10.0	241	4	US-09-604-287A-323 Sequence 323, App
20	237	10.0	241	4	US-09-834-759-323 Sequence 323, App
21	226.2	9.5	239	2	US-08-892-880-14 Sequence 14, Appl
22	191.4	8.1	466	2	US-08-892-880-13 Sequence 13, Appl
23	160	6.7	498	2	US-08-892-880-15 Sequence 15, Appl
24	55.4	2.3	7218	1	US-08-232-463-14 Sequence 14, Appl
25	51.2	2.2	724	3	US-08-998-416-683 Sequence 683, App
26	50	2.1	50	4	US-09-907-794A-205 Sequence 205, App
27	50	2.1	50	4	US-09-905-125A-205 Sequence 205, App

28	50	2.1	50	4	US-09-902-775A-205 Sequence 205, App
29	49.2	2.1	663	3	US-08-998-416-191 Sequence 191, App
30	49.2	2.1	732	3	US-08-998-416-1036 Sequence 1036, App
31	49.2	2.1	854	3	US-08-998-416-534 Sequence 534, App
32	48.8	2.1	860	3	US-08-998-416-287 Sequence 287, App
33	48.4	2.0	640681	4	US-09-790-988-1 Sequence 1, Appli
34	48.2	2.0	1587	4	US-09-010-147B-19 Sequence 19, Appl
35	48.2	2.0	1720	4	US-09-148-545-53 Sequence 53, Appl
36	46.6	2.0	3207	1	US-07-946-497-1 Sequence 1, Appli
37	46.6	2.0	3207	1	US-08-483-322-1 Sequence 1, Appli
38	46.6	2.0	3207	2	US-08-478-882-1 Sequence 1, Appli
39	46.4	2.0	6040	4	US-10-204-708-70 Sequence 70, Appl
40	46	1.9	832	4	US-09-621-976-2813 Sequence 2813, Ap
41	46	1.9	3057	4	US-09-601-198-55 Sequence 55, Appl
42	46	1.9	6113	4	US-10-204-708-13 Sequence 13, Appl
43	45.8	1.9	319608	4	US-09-539-333D-1 Sequence 1, Appli
44	45.8	1.9	319608	4	US-09-679-409-1 Sequence 1, Appli
45	45.6	1.9	6265	4	US-09-129-112-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-907-794A-200
; Sequence 200, Application US/09907794A
; Patent No. 6635468

GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-794A-200

Query Match 100.0%; Score 2372; DB 4; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 AGCAGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60
QY 61 GTTCCAGAACTCTCCATCCGACTAGTTATTAGCATCTGCCTCTCATATCACCAGTGGC 120
Db 61 GTTCCAGAACTCTCCATCCGACTAGTTATTAGCATCTGCCTCTCATATCACCAGTGGC 120
QY 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTACGCCTG 180
Db 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTACGCCTG 180
QY 181 GTGTTGCTTCTCACTTCCATCTGGACCAAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
Db 181 GTGTTGCTTCTCACTTCCATCTGGACCAAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
QY 241 GAAGAGCTTTCCATCCAGGTGTCATGCAAGATTATGGGATCACCCTTGTGAGCAAAAAG 300
Db 241 GAAGAGCTTTCCATCCAGGTGTCATGCAAGATTATGGGATCACCCTTGTGAGCAAAAAG 300
QY 301 GCGAACCCAGCAGCTGAATTTACAGAACTAAGGAGGCTGTAGGCTGCTGGACTAAGT 360
Db 301 GCGAACCCAGCAGCTGAATTTACAGAACTAAGGAGGCTGTAGGCTGCTGGACTAAGT 360
QY 361 TTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420
Db 361 TTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420
QY 421 GGCTGGTGGAGATGGATTGCTGCTCATCTTAGGATTAGCCCAACCCCAAGTGTGGG 480
Db 421 GGCTGGTGGAGATGGATTGCTGCTCATCTTAGGATTAGCCCAACCCCAAGTGTGGG 480
QY 481 AAAAATGGGTGGGTGTCCTGATTTGGAAGTTCCAGTGGCCGACAGTTTGCAGCCTAT 540
Db 481 AAAAATGGGTGGGTGTCCTGATTTGGAAGTTCCAGTGGCCGACAGTTTGCAGCCTAT 540
QY 541 TGTACAACTCATCTGATACCTTGGACTAACTCGTGATTCAGAAATATCACCACCAAA 600
Db 541 TGTACAACTCATCTGATACCTTGGACTAACTCGTGATTCAGAAATATCACCACCAAA 600
QY 601 GATCCCATATTCAACACTCAACTGCAACACAAACAGAAATTTATTGTGAGTGACAGT 660
Db 601 GATCCCATATTCAACACTCAACTGCAACACAAACAGAAATTTATTGTGAGTGACAGT 660

QY 661 ACCTACTCGTGGCATCCCCTTACTTACAATACCTGCCCTACTACTCTCCTCTGCT 720
Db 661 ACCTACTCGTGGCATCCCCTTACTTACAATACCTGCCCTACTACTCTCCTCTGCT 720
QY 721 CCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATTGTGTGACAGAAAGTTTATG 780
Db 721 CCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATTGTGTGACAGAAAGTTTATG 780
QY 781 GAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAAAATAAGCAGCATCAAG 840
Db 781 GAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAAAATAAGCAGCATCAAG 840
QY 841 AATGAAGCTGCTGGTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGTGCTCCTCTTC 900
Db 841 AATGAAGCTGCTGGTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGTGCTCCTCTTC 900
QY 901 TTTGGTGTGCAGCTGGTCTTGGATTTTGTATGTCAAAAGGTATGTAAGGCTTCCCT 960
Db 901 TTTGGTGTGCAGCTGGTCTTGGATTTTGTATGTCAAAAGGTATGTAAGGCTTCCCT 960
QY 961 TTTACAAACAAGATCAGAGAAAGAAATGATCGAAACCAAGTAGTAAAGGAGGAG 1020
Db 961 TTTACAAACAAGATCAGAGAAAGAAATGATCGAAACCAAGTAGTAAAGGAGGAG 1020
QY 1021 GCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACTGATAAAACCCAGAGATCC 1080
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QY 1081 AAGAGTCCAAAGCAAACTACCGTCCGATGCCGTGGAAGCTGAAAGTTAGATGAGACAG 1140
Db 1081 AAGAGTCCAAAGCAAACTACCGTCCGATGCCGTGGAAGCTGAAAGTTAGATGAGACAG 1140
QY 1141 TGAGGAGACACACCTGAGGCTGGTTCTTTTATGCTCCTTACCTGCCCGAGTGGGAA 1200
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QY 1201 ATCAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCCCTAAGTGAATCAGC 1260
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QY 1261 TCAGGACTGCCATGGACTATGGAGTGCAACAAAGAGAAATGCCCTTCTCTTATTTAAAC 1320
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QY 1441 TCATCAGTATCCAGTGGTAAAGGCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1500
Db 1441 TCATCAGTATCCAGTGGTAAAGGCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1500
QY 1501 CAAGGACTCACTGAGACCAAGGCTTCTTACTGATTCGAGCTCAGACCTTCTTCA 1560
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QY 1561 GCTCTGAAAGAGAAACCGTATCCACCTGACATGTCTTCTGAGCCCGTAAAGCAAA 1620
Db 1561 GCTCTGAAAGAGAAACCGTATCCACCTGACATGTCTTCTGAGCCCGTAAAGCAAA 1620
QY 1621 AGAATGGCAGAAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATACTTGAGACCTAA 1680
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QY 1741 GCAGGAGCTGTAAACACACAGACAGGCTCAAGTGTCTCTCTGAAACACATTGAGTTGGAAT 1800
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1741 GCAGGAGCTGTAAACACACAGACAGGCTCAAGTGTCTCTCTGAAACACATTGAGTTGGAAT 1800
QY 1801 CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1801 CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860
QY 1861 AGGAAATATATCTTTTACAAGTAACAAAAATAAAACTCTTATAAAATTTCTATTTTATCT 1920
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1861 AGGAAATATATCTTTTACAAGTAACAAAAATAAAACTCTTATAAAATTTCTATTTTATCT 1920
QY 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
QY 1981 TTCAACAAACATTTTGTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTC 2040
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1981 TTCAACAAACATTTTGTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTC 2040
QY 2041 TGTAAATTGAATATTTCTCTCAAAAAATTTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
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2041 TGTAAATTGAATATTTCTCTCAAAAAATTTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
QY 2101 TTTTTCAGTTTGTGATTTCTTAGCTTATCTACTTCCAAACTAATTTTATTTTGCTGA 2160
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2101 TTTTTCAGTTTGTGATTTCTTAGCTTATCTACTTCCAAACTAATTTTATTTTGCTGA 2160
QY 2161 GACTAATCTTATTCATTTCT 2220
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2161 GACTAATCTTATTCATTTCT 2220
QY 2221 ATACCTAAGAACTACATTTGTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2280
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2221 ATACCTAAGAACTACATTTGTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2280
QY 2281 CAAATGTATCACTAGCCCT 2340
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2281 CAAATGTATCACTAGCCCT 2340
QY 2341 TGTGACAAAAAATTAAGCAATTTAGAAAACTT 2372
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2341 TGTGACAAAAAATTAAGCAATTTAGAAAACTT 2372

RESULT 2

US-09-905-125A-200
; Sequence 200, Application US/09905125A
; Patent No. 6664376

GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/905,125A

; CURRENT FILING DATE: 2001-07-12

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

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; PRIOR FILING DATE: 1999-09-15

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; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/28565

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: PCT/US99/30911

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219

; PRIOR FILING DATE: 2000-01-05

; NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 200

; LENGTH: 2372

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-905-125A-200

Query Match 100.0%; Score 2372; DB 4; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCAGGGAAATCCGGATGTCGGTTATGAAAGTGAGCAGTGAGTGTGAGCCTCAACATA 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 AGCAGGGAAATCCGGATGTCGGTTATGAAAGTGAGCAGTGAGTGTGAGCCTCAACATA 60
QY 61 GTTCCAGAACTCTCCATCCGGAAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 GTTCCAGAACTCTCCATCCGGAAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
QY 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
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121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
QY 181 GTGTTGCTTCTCATTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 GTGTTGCTTCTCATTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
QY 241 GAAGAGCTTTCATCCAGGTGTGATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAG 300
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241 GAAGAGCTTTCATCCAGGTGTGATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAG 300
QY 301 GCGAACCAACAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCCCTGTAGGCTGCTGGACTAAGT 360

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; PRIOR FILING DATE: 1999-07-07
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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-902-775A-200

Query Match 100.0%; Score 2372; DB 4; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AGCAGGAAATCCGGATGTCCTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA	60
Db	1	AGCAGGAAATCCGGATGTCCTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA	60
QY	61	GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCTCATATCACCAGTGGC	120
Db	61	GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCTCATATCACCAGTGGC	120
QY	121	CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCAGGTGCTTCAGCCTG	180
Db	121	CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCAGGTGCTTCAGCCTG	180
QY	181	GTGTTGCTTCTCACTTCGACACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA	240
Db	181	GTGTTGCTTCTCACTTCGACACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA	240
QY	241	GAAGAGCTTTCATCCAGGTGTCAATGACAGAAATATGGGATCACCCCTTGTGAGCAAAAAG	300
Db	241	GAAGAGCTTTCATCCAGGTGTCAATGACAGAAATATGGGATCACCCCTTGTGAGCAAAAAG	300
QY	301	GCGAACCCAGCAGCTGAATTTACAGAACTAAGGAGGCCTGTAGGCTGCTGGGACTAAGT	360
Db	301	GCGAACCCAGCAGCTGAATTTACAGAACTAAGGAGGCCTGTAGGCTGCTGGGACTAAGT	360
QY	361	TTGGCCGGCAAGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	420
Db	361	TTGGCCGGCAAGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	420
QY	421	GGCTGGGTTGGAGATGGATTCTGTGGTCACTCTAGGATTAGCCCAACCCCAAGTGTGGG	480
Db	421	GGCTGGGTTGGAGATGGATTCTGTGGTCACTCTAGGATTAGCCCAACCCCAAGTGTGGG	480
QY	481	AAAAATGGGTGGGTGTCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	540
Db	481	AAAAATGGGTGGGTGTCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	540
QY	541	TGTTACAACTCATCTGATACTTGGACTAATCGTGCATTCCAGAAATATCACCAACCAAA	600
Db	541	TGTTACAACTCATCTGATACTTGGACTAATCGTGCATTCCAGAAATATCACCAACCAAA	600
QY	601	GATCCCATATTCACACTCAAACTGCAACACAAACAGAAATTTATTGTTCAGTGACAGT	660
Db	601	GATCCCATATTCACACTCAAACTGCAACACAAACAGAAATTTATTGTTCAGTGACAGT	660
QY	661	ACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCCCTACTACTCTCCTGCT	720
Db	661	ACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCCCTACTACTCTCCTGCT	720
QY	721	CCAGCTTCCACTTCTATTCCACGGAGAAAAAATGATTGTGTACAGAAAGTTTTTATG	780
Db	721	CCAGCTTCCACTTCTATTCCACGGAGAAAAAATGATTGTGTACAGAAAGTTTTTATG	780
QY	781	GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCAATCAAG	840
Db	781	GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCAATCAAG	840
QY	841	AATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTCTCTCCTCTTC	900
Db	841	AATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTCTCTCCTCTTC	900
QY	901	TTTGGTGTGCAGCTGCTTGGATTGTTGCTATGTCAAAGGTATGTGAAGGCCCTTCCCT	960
Db	901	TTTGGTGTGCAGCTGCTTGGATTGTTGCTATGTCAAAGGTATGTGAAGGCCCTTCCCT	960
QY	961	TTTACAAAACAAGAAATCAGCAGAAAGAAATGATCGAAAAACCAAAAGTAGTAAAGGAGAG	1020
Db	961	TTTACAAAACAAGAAATCAGCAGAAAGAAATGATCGAAAAACCAAAAGTAGTAAAGGAGAG	1020
QY	1021	GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACTGATAAAAAACCCAGAGAGTCC	1080
Db	1021	GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACTGATAAAAAACCCAGAGAGTCC	1080


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QY 1081 AAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140
Db 1081 AAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140
QY 1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCCTGCCCCAGCTGGGAA 1200
Db 1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCCTGCCCCAGCTGGGAA 1200
QY 1201 ATCAAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACCCCTGGTTCCTAACTGGAATCAGC 1260
Db 1201 ATCAAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACCCCTGGTTCCTAACTGGAATCAGC 1260
QY 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGATGCCCTTCTCCTTATTGTAAC 1320
Db 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGATGCCCTTCTCCTTATTGTAAC 1320
QY 1321 CCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT 1380
Db 1321 CCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT 1380
QY 1381 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTTGCAAGTCAAGGACCTAAACATC 1440
Db 1381 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTTGCAAGTCAAGGACCTAAACATC 1440
QY 1441 TCATCAGTATCCAGTGTGTAAGAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGC 1500
Db 1441 TCATCAGTATCCAGTGTGTAAGAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGC 1500
QY 1501 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATCCGAGCTCAGACCCCTTCTTCA 1560
Db 1501 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATCCGAGCTCAGACCCCTTCTTCA 1560
QY 1561 GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA 1620
Db 1561 GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA 1620
QY 1621 AGAATGGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680
Db 1621 AGAATGGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680
QY 1681 TCTCTGTAAAGCTAAAATAAGAAATAGAACACAGGCTGAGGATACGACAGTACACTGTCA 1740
Db 1681 TCTCTGTAAAGCTAAAATAAGAAATAGAACACAGGCTGAGGATACGACAGTACACTGTCA 1740
QY 1741 GCAGGGACTGTAAACACACAGACAGGGTCAAAGTGTCTTCTGAAACACATGAGTTGGAAT 1800
Db 1741 GCAGGGACTGTAAACACACAGACAGGGTCAAAGTGTCTTCTGAAACACATGAGTTGGAAT 1800
QY 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860
Db 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860
QY 1861 AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1920
Db 1861 AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1920
QY 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAA 1980
Db 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAA 1980
QY 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTC 2040
Db 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTC 2040
QY 2041 TGTAAATTGAATATTATTCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
Db 2041 TGTAAATTGAATATTATTCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
QY 2101 TTTTTTTCAGTTTGTATATTTCTAGCTTATCTACTTCCAAACCTAATTTTATTGCTGA 2160
Db 2101 TTTTTTTCAGTTTGTATATTTCTAGCTTATCTACTTCCAAACCTAATTTTATTGCTGA 2160
QY 2161 GACTAATCTTATTTCTCTAATAATGGCAACCAATTATAACCTTAATTTATTATTAAC 2220
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Db 2161 GACTAATCTTATTCTCTAATAATGGCAACCAATTATAACCTTAATTTATTATTAAC 2220
QY 2221 ATACCTAAGAAGTACATTGTTACCTCTATATACCAAGCACATTTTAAAAAGTGCCATTAA 2280
Db 2221 ATACCTAAGAAGTACATTGTTACCTCTATATACCAAGCACATTTTAAAAAGTGCCATTAA 2280
QY 2281 CAAATGTATCACTAGCCCTCCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAAATATT 2340
Db 2281 CAAATGTATCACTAGCCCTCCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAAATATT 2340
QY 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372
Db 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372

RESULT 4
US-09-833-381-849
; Sequence 849, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 849
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-849

Query Match      100.0%; Score 2372; DB 4; Length 2404;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCAGGGAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60
Db 31 AGCAGGGAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 90
QY 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCTCATATCACCAGTGGC 120
Db 91 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCTCATATCACCAGTGGC 150
QY 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
Db 151 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 210
QY 181 GTGTTGCTTCTCACTTCCATCTGGACCAAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
Db 211 GTGTTGCTTCTCACTTCCATCTGGACCAAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 270
QY 241 GAAGAGCTTTCATCCAGGTGTCAATGAGAACTATGGGATCACCCCTGTGAGCAAAAAG 300
Db 271 GAAGAGCTTTCATCCAGGTGTCAATGAGAACTATGGGATCACCCCTGTGAGCAAAAAG 330
QY 301 GCGAACCAAGCAGCTGAATTTACAGAACTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGT 360
Db 331 GCGAACCAAGCAGCTGAATTTACAGAACTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGT 390
QY 361 TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420
Db 391 TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 450
QY 421 GGCTGGGTTGGAGATGGATTTCGTGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGG 480
Db 451 GGCTGGGTTGGAGATGGATTTCGTGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGG 510
QY 481 AAAATGGGGTGGGTGTCTCGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
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Db 511 AAAAAAAAAAAGGGTGTCTGATTTTGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 570
QY 541 TGTACAACTCATCTGATACCTTGACTAACTCGTGCAATCCAGAAATATCACCACCAAA 600
Db 571 TGTACAACTCATCTGATACCTTGACTAACTCGTGCAATCCAGAAATATCACCACCAAA 630
QY 601 GATCCCATATTCAAACACTCAAACTGCAACACAAACAAACAGAAATTTATTTGTCAGTGACGT 660
Db 631 GATCCCATATTCAAACACTCAAACTGCAACACAAACAAACAGAAATTTATTTGTCAGTGACGT 690
QY 661 ACCTACTCGGTGGCATCCCTTTACTCTACAAATACCTGCCCCCTACTACTACTCTCCTGCT 720
Db 691 ACCTACTCGGTGGCATCCCTTTACTCTACAAATACCTGCCCCCTACTACTACTCTCCTGCT 750
QY 721 CCAGCTTCCACTTCTATTTCCACGGAGAAAATAATTGATTTGTGTCAAGAAATTTTATG 780
Db 751 CCAGCTTCCACTTCTATTTCCACGGAGAAAATAATTGATTTGTGTCAAGAAATTTTATG 810
QY 781 GAAACTAGCACCAATGCTACAGAAACTGAACCAATTTGTGAAAATAAAGCAGCATTC AAG 840
Db 811 GAAACTAGCACCAATGCTACAGAAACTGAACCAATTTGTGAAAATAAAGCAGCATTC AAG 870
QY 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTGCTCTCTCTTC 900
Db 871 AATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTGCTCTCTCTTC 930
QY 901 TTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTC AAAAGGTATGTGAAGGCTTCCCT 960
Db 931 TTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTC AAAAGGTATGTGAAGGCTTCCCT 990
QY 961 TTTACAAACAAGAAATCAGCAGAAAGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAAG 1020
Db 991 TTTACAAACAAGAAATCAGCAGAAAGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAAG 1050
QY 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAAGAAACTGATAAAAAACCCAGAAAGTCC 1080
Db 1051 GCCAATGATAGCAACCTTAATGAGGAATCAAAGAAACTGATAAAAAACCCAGAAAGTCC 1110
QY 1081 AAGAGTCCAAGCAAAACTACCGTGCATGCCGTGGAAGTGAAGTTAGATGAGACAGAAA 1140
Db 1111 AAGAGTCCAAGCAAAACTACCGTGCATGCCGTGGAAGTGAAGTTAGATGAGACAGAAA 1170
QY 1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCTTACCTGCCCCAGCTGGGAA 1200
Db 1171 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCTTACCTGCCCCAGCTGGGAA 1230
QY 1201 ATCAAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACCCCTTGGTTCCCTAACTGGAATCAGC 1260
Db 1231 ATCAAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACCCCTTGGTTCCCTAACTGGAATCAGC 1290
QY 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTTGTAAC 1320
Db 1291 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTTGTAAC 1350
QY 1321 CCTGTCTGGATCCTATCCTTACCTTCCAAAGCTTCCACGGCTTTCTAGCCTGGCTAT 1380
Db 1351 CCTGTCTGGATCCTATCCTTACCTTCCAAAGCTTCCACGGCTTTCTAGCCTGGCTAT 1410
QY 1381 GTCTTAATAATATCCCACCTGGGAGAAAGGAGTTTTCGAAAAGTCAAGGACCTAAAAACATC 1440
Db 1411 GTCTTAATAATATCCCACCTGGGAGAAAGGAGTTTTCGAAAAGTCAAGGACCTAAAAACATC 1470
QY 1441 TCATCAGTATCCAGTGGTAAAAAGGCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1500
Db 1471 TCATCAGTATCCAGTGGTAAAAAGGCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1530
QY 1501 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGGCAGCTCAGACCCCTTTCTTCA 1560
Db 1531 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGGCAGCTCAGACCCCTTTCTTCA 1590
QY 1561 GCTCTGAAAGAGAAAAACAGTATCCACCTGACATGTCTTCTGAGCCCGGTAAGAGCAAA 1620

Db 1591 GCTCTGAAAGAGAAAAACACGATATCCACCTGACATGTCTTCTGAGCCCGGTAAGAGCAA 1650
QY 1621 AGAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTATAAATTGAGACCTAA 1680
Db 1651 AGAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTATAAATTGAGACCTAA 1710
QY 1681 TCTCTGTAAGCTAAAAATAAAGAAATAGAAACAAGGCTGAGGATACGAGTACGACTGTCA 1740
Db 1711 TCTCTGTAAGCTAAAAATAAAGAAATAGAAACAAGGCTGAGGATACGAGTACGACTGTCA 1770
QY 1741 GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTCTGTAACACATTGAGTTGGAAT 1800
Db 1771 GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTCTGTAACACATTGAGTTGGAAT 1830
QY 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACCTGCTGATATTTCTCT 1860
Db 1831 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACCTGCTGATATTTCTCT 1890
QY 1861 AGGAAATATACTTTTACAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1920
Db 1891 AGGAAATATACTTTTACAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1950
QY 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
Db 1951 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 2010
QY 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTAATACACTC 2040
Db 2011 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTAATACACTC 2070
QY 2041 TGTAAATTGAATATTTCTCTCAAAAAATTTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
Db 2071 TGTAAATTGAATATTTCTCTCAAAAAATTTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2130
QY 2101 TTTTTCAGTTTGATATTTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTGTCTGA 2160
Db 2131 TTTTTCAGTTTGATATTTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTGTCTGA 2190
QY 2161 GACTAATCTTATTCATTTTCTCTAATATGGCAACCATTAACCTTAATTTATTTAATTAAC 2220
Db 2191 GACTAATCTTATTCATTTTCTCTAATATGGCAACCATTAACCTTAATTTATTTAATTAAC 2250
QY 2221 ATACCTAAGAAGTACATTTTACCTCTATATACCAAGACACATTTTAAAAAGTGCCATTA 2280
Db 2251 ATACCTAAGAAGTACATTTTACCTCTATATACCAAGACACATTTTAAAAAGTGCCATTA 2310
QY 2281 CAAATGTATCACTAGCCCTCCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAATATT 2340
Db 2311 CAAATGTATCACTAGCCCTCCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAATATT 2370
QY 2341 TGTGACAAAAAATTAAGCATTTAGAAAACTT 2372
Db 2371 TGTGACAAAAAATTAAGCATTTAGAAAACTT 2402

RESULT 5
US-09-833-381-853
; Sequence 853, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 853
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-833-381-853

Query Match 100.0%; Score 2372; DB 4; Length 2404;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	AGCAGGGAATCCGAGTCTCGGTATGAAGTGGAGCAGTGAAGTGGAGCCTCAACATA	60						
Db	31	AGCAGGGAATCCGAGTCTCGGTATGAAGTGGAGCAGTGAAGTGGAGCCTCAACATA	90						
QY	61	GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCTCTCATATCACCAGTGC	120						
Db	91	GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCTCTCATATCACCAGTGC	150						
QY	121	CATCTGAGGTGTTTCCCTGCTCTGAAGGGTAGGCACGATGGCCAGGTCTTCAGCCTG	180						
Db	151	CATCTGAGGTGTTTCCCTGCTCTGAAGGGTAGGCACGATGGCCAGGTCTTCAGCCTG	210						
QY	181	GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGA	240						
Db	211	GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGA	270						
QY	241	GAAGAGCTTTCATCCAGTGTATGCAGAAATTATGGGATCACCTTGTGAGCAAAAAG	300						
Db	271	GAAGAGCTTTCATCCAGTGTATGCAGAAATTATGGGATCACCTTGTGAGCAAAAAG	330						
QY	301	GCGAACAGCAGCTGAATTCACAGAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGT	360						
Db	331	GCGAACAGCAGCTGAATTCACAGAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGT	390						
QY	361	TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAACTTGACGCTAT	420						
Db	391	TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAACTTGACGCTAT	450						
QY	421	GGCTGGGTTGGAGATGGATTCTGTTGTCATCTCTAGGATTAGCCAAACCCCAAGTGGG	480						
Db	451	GGCTGGGTTGGAGATGGATTCTGTTGTCATCTCTAGGATTAGCCAAACCCCAAGTGGG	510						
QY	481	AAAAATGGGTGGTCTCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	540						
Db	511	AAAAATGGGTGGTCTCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	570						
QY	541	TGTTACAACTCATCTGATCTTGGAATACTCGTGCAATCCAGAAATTATCACCACCAA	600						
Db	571	TGTTACAACTCATCTGATCTTGGAATACTCGTGCAATCCAGAAATTATCACCACCAA	630						
QY	601	GATCCCATATTCAACTCAAACTGCAACACAAACAAACAGAAATTTATGTCAGTGACAGT	660						
Db	631	GATCCCATATTCAACTCAAACTGCAACACAAACAAACAGAAATTTATGTCAGTGACAGT	690						
QY	661	ACCTACTCGGTGGATCCCTTACTCTACAAATACCTGCCCTACTACTCTCTCTGCT	720						
Db	691	ACCTACTCGGTGGATCCCTTACTCTACAAATACCTGCCCTACTACTCTCTCTGCT	750						
QY	721	CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAATTTTATG	780						
Db	751	CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAATTTTATG	810						
QY	781	GAAGCTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAATTAAGCAGCATTCAG	840						
Db	811	GAAGCTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAATTAAGCAGCATTCAG	870						
QY	841	AATGAAGCTGCTGGGTTTGGAGGTGTCACGCTCTGCTAGTGTGCTCTCTCTCTTC	900						
Db	871	AATGAAGCTGCTGGGTTTGGAGGTGTCACGCTCTGCTAGTGTGCTCTCTCTCTTC	930						
QY	901	TTTGGTGTGAGCTGGTCTTGGATTTTGGATTTTGGATTTTGGATTTTGGATTTTGGAT	960						
Db	931	TTTGGTGTGAGCTGGTCTTGGATTTTGGATTTTGGATTTTGGATTTTGGATTTTGGAT	990						
QY	961	TTTACAAACAAGAAATCAGCAGAAGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAG	1020						
Db	991	TTTACAAACAAGAAATCAGCAGAAGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAG	1050						

QY	1021	GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACTGATFAAAAAACCAGAGAGTCC	1080
Db	1051	GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACTGATFAAAAAACCAGAGAGTCC	1110
QY	1081	AAGAGTCCAAAGCAAAACTACCGTCCGATGCCTGGAAGCTGAAAGTTTAGATGAGACAGAAA	1140
Db	1111	AAGAGTCCAAAGCAAAACTACCGTCCGATGCCTGGAAGCTGAAAGTTTAGATGAGACAGAAA	1170
QY	1141	TGAGGAGACACACCTGAGGCTGGTTTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1200
Db	1171	TGAGGAGACACACCTGAGGCTGGTTTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1230
QY	1201	ATCAAAAGGGCCCAAGAACCAAGAAAGAAAGTCCACCCCTTGGTTCTTAAGTGAATCAGC	1260
Db	1231	ATCAAAAGGGCCCAAGAACCAAGAAAGAAAGTCCACCCCTTGGTTCTTAAGTGAATCAGC	1290
QY	1261	TCAGGACTGCCATTGGACTATGGAGTGCAACCAAGAGAAATGCCCTTCTCTTATTGTAAC	1320
Db	1291	TCAGGACTGCCATTGGACTATGGAGTGCAACCAAGAGAAATGCCCTTCTCTTATTGTAAC	1350
QY	1321	CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT	1380
Db	1351	CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT	1410
QY	1381	GTCTTAATAATATCCACTGGGAGAAAGGAGTTTTCGAAAGTCAAGGACCTAAACATC	1440
Db	1411	GTCTTAATAATATCCACTGGGAGAAAGGAGTTTTCGAAAGTCAAGGACCTAAACATC	1470
QY	1441	TCATCAGTATCCAGTGGTAAAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC	1500
Db	1471	TCATCAGTATCCAGTGGTAAAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC	1530
QY	1501	CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTTCCGAGCTCAGACCCCTTTCTTCA	1560
Db	1531	CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTTCCGAGCTCAGACCCCTTTCTTCA	1590
QY	1561	GCTCTGAAAGAGAAACACGATATCCCACTGACATGTCTTCTGAGCCCGGTAAAGAGCAAA	1620
Db	1591	GCTCTGAAAGAGAAACACGATATCCCACTGACATGTCTTCTGAGCCCGGTAAAGAGCAAA	1650
QY	1621	AGAAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTGAGACCTAA	1680
Db	1651	AGAAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTGAGACCTAA	1710
QY	1681	TCTCTGTAAGCTAAAAATAAAGAAATAGAAAGGCTGAGGATACGACAGTACACTGTCA	1740
Db	1711	TCTCTGTAAGCTAAAAATAAAGAAATAGAAAGGCTGAGGATACGACAGTACACTGTCA	1770
QY	1741	GCAGGACTGTAAAAACACAGACAGGCTCAAAGTGTCTTCTCTGAACACATTTGAGTTGGAAT	1800
Db	1771	GCAGGACTGTAAAAACACAGACAGGCTCAAAGTGTCTTCTCTGAACACATTTGAGTTGGAAT	1830
QY	1801	CACCTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT	1860
Db	1831	CACCTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT	1890
QY	1861	AGGAAATATATCTTTTACAAGTAAACAAAAATAAAAACTCTTATAAATTTCTATTTATCT	1920
Db	1891	AGGAAATATATCTTTTACAAGTAAACAAAAATAAAAACTCTTATAAATTTCTATTTATCT	1950
QY	1921	GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTAAAAAGTAATAAAA	1980
Db	1951	GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTAAAAAGTAATAAAA	2010
QY	1981	TTCAACAAACATTTGCTGAATAGTACTATATGTCAAGTGTCTGCAAGGTATTACACTC	2040
Db	2011	TTCAACAAACATTTGCTGAATAGTACTATATGTCAAGTGTCTGCAAGGTATTACACTC	2070
QY	2041	TGTAATTGAATATATTCTCAAAAAATTCACATAGTAGAACGCTATCTGGGAAGCTAT	2100
Db	2071	TGTAATTGAATATATTCTCAAAAAATTCACATAGTAGAACGCTATCTGGGAAGCTAT	2130

QY 2101 TTTTTCAGTTTTCAGATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTTTGTCTGA 2160
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Db 2131 TTTTTCAGTTTTCAGATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTTTGTCTGA 2190
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QY 2161 GACTAATCTTATTCATTTTCTCTAATATGGCAACCATTATAACCTTAAATTTATTTAATTAAC 2220
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Db 2191 GACTAATCTTATTCATTTTCTCTAATATGGCAACCATTATAACCTTAAATTTATTTAATTAAC 2250
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QY 2221 ATACCTAAGAAGTACATTTGTTACCTCTATATACCAAGCACATTTTAAAAGTGCCATTAA 2280
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Db 2251 ATACCTAAGAAGTACATTTGTTACCTCTATATACCAAGCACATTTTAAAAGTGCCATTAA 2310
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QY 2281 CAAATGTATTCAGTACGCTCCTTTTCCAAACAAGAGGGAAGTGAAGATGCAGAAATATT 2340
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Db 2311 CAAATGTATTCAGTACGCTCCTTTTCCAAACAAGAGGGAAGTGAAGATGCAGAAATATT 2370
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QY 2341 TGTGACAAAAAATTAAGCATTTAGAAAACTT 2372
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Db 2371 TGTGACAAAAAATTAAGCATTTAGAAAACTT 2402
|||

RESULT 6

US-08-892-880-1
; Sequence 1, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2313 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..1056
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 154..1056
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 91..153

US-08-892-880-1
Query Match 96.6%; Score 2290.2; DB 2; Length 2313;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2292; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 75 CATCCGGACTAGTTATTGAGCATCTGCCCTCTCATATCACCAGTGGCCATCTGAGGTGTTT 134
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Db 6 CATCCGGACTAGTTATTGAGCATCTGCCCTCTCATATCACCAGTGGCCATCTGAGGTGTTT 65
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QY 135 CCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGTTCTCTCAC 194
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Db 66 CCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGTTCTCTCAC 125
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QY 195 TTCCATCTGGACCACGAGGCTCCTGGTCCAAAGGCTCTTTCGTCGAGAACGCAACAGCAGCT 254
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Db 126 TTCCATCTGGACCACGAGGCTCCTGGTCCAAAGGCTCTTTCGTCGAGAACGCAACAGCAGCT 185
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QY 255 CCAGGTGTCTATGCAGAAATTATGGGGATCACCCCTGTGAGCAAAAAGGCGCAACAGCAGCT 314
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Db 186 CCAGGTGTCTATGCAGAAATTATGGGGATCACCCCTGTGAGCAAAAAGGCGCAACAGCAGCT 245
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QY 315 GAATTTACAGAACTAAGGAGGCTGTAGGCTGTGGGACTTAAGTTTGGCCGGCAAGGA 374
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Db 246 GAATTTACAGAACTAAGGAGGCTGTAGGCTGTGGGACTTAAGTTTGGCCGGCAAGGA 305
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QY 375 CCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGA 434
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Db 306 CCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGCAACTTGCAGCTATGGCTGGGTGGCGA 365
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QY 435 TGGATTGCTGGTCACTCTTAGGATTAGCCCAACCCCAAGTGTGGGAAAATGGGGTGGG 494
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Db 366 TGGATTGCTGGTCACTCTTAGGATTAGCCCAACCCCAAGTGTGGGAAAATGGGGTGGG 425
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QY 495 TGTCTGTATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATC 554
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Db 426 TGTCTGTATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATC 485
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QY 555 TGATACTTGGACTAACTCGTGCATTCCAGAAATATATCACCACCAAGATCCCATATTCAA 614
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Db 486 TGATACTTGGACTAACTCGTGCATTCCAGAAATATATCACCACCAAGATCCCATATTCAA 545
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QY 615 CACTCAAACTGCAACACAAACAACAGAAATTTATGTCAGTGACAGTACCTACTCGGTGGC 674
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Db 546 CACTCAAACTGCAACACAAACAACAGAAATTTATGTCAGTGACAGTACCTACTCGGTGGC 605
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QY 675 ATCCCCCTTACTCTACAATACCTGCCCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTC 734
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Db 606 ATCCCCCTTACTCTACAATACCTGCCCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTC 665
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QY 735 TATTCCACGGAGAAAAAATGATTTGTGTGCACAGAGTTTATGGAACCTAGCACCAT 794
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Db 666 TATTCCACGGAGAAAAAATGATTTGTGTGCACAGAGTTTATGGAACCTAGCACCAT 725
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QY 795 GTCTACAGAAACTGAACCATTTGTTGAAAATAAAGCAGCATTTCAAGAAATGAAGTGTGG 854
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Db 726 GTCTACAGAAACTGAACCATTTGTTGAAAATAAAGCAGCATTTCAAGAAATGAAGTGTGG 785
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QY 855 GTTTGGAGGTGTCCCAAGGCTCTGTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 914
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QY 1095 AACTACCGTGCATGCCCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACC 1154
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QY 1026 AACTACCGTGCATGCCCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACC 1085
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QY 1155 TGAGGCTGGTTTCTTTTCATGCTCCTTACCCCTGCCCCAGCTGGGAAATCAAAAGGGCCAA 1214
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QY 1086 TGAGGCTGGTTTCTTTCAAGCTCCTTACCCCTGCCCCAGCTGGGAAATCAAAAGGGCCAA 1145
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QY 1215 AGAACCAAGAAGAAAGTCCACCCCTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATT 1274
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QY 1146 AGAACCAAGAAGAAAGTCCACCCCTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATT 1205
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QY 1275 GGACTATGGAGTGCACCAAGAGAATGCCCTTCTCCCTTATGTAAACCCCTGTCTGGATCCT 1334
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QY 1206 GGACTATGGAGTGCACCAAGAGAATGCCCTTCTCCCTTATGTAAACCCCTGTCTGGATCCT 1265
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QY 1335 ATCCTCCTACCTCCAAAGCTTCCACGGCCTTCTAGCTGGCTATGTCTCTAATAATATC 1394
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QY 1266 ATCCTCCTACCTCCAAAGCTTCCACGGCCTTCTAGCTGGCTATGTCTCTAATAATATC 1325
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QY 1395 CCACTGGGAGAAAGGAGTTTGCAAAGTGCAAGGACTPAAAAATCTCATCAGTATCCAG 1454
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QY 1326 CCACTGGGAGAAAGGAGTTTGCAAAGTGCAAGGACTPAAAAATCTCATCAGTATCCAG 1385
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QY 1455 TGGTAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGCCAAAGGAGTCACTGA 1514
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QY 1386 TGGTAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGCCAAAGGAGTCACTGA 1445
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QY 1515 GACCAAGGCTTCTCTACTGATTCGCAGCTCAGACCCCTTCTCAGCTCTGAAAGAGAA 1574
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QY 1446 GACCAAGGCTTCTCTACTGATTCGCAGCTCAGACCCCTTCTCAGCTCTGAAAGAGAA 1505
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QY 1575 ACACGTATCCACCTGACATGTCTTCTGAGCCCGTAAAGAGCAGCAAAAGAAATGGCAGAAAA 1634
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QY 1626 AAATAAGAAATAGAACAGGCTGAGGATACGAGTACGACGTGTCAGCAGGGAAGTGTAAA 1685
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QY 1815 CACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCTAGGAAATATACTTT 1874
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QY 1875 TACAAGTAACAAAAATAAAAACTCTTATAAAATTTCTATTTTATCTGAGTTACAGAAAATG 1934
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QY 1806 TACAAGTAACAAAAATAAAAACTCTTATAAAATTTCTATTTTATCTGAGTTACAGAAAATG 1865
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QY 1935 ATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCACAAACATTT 1994
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QY 1866 ATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCACAAACATTT 1925
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QY 1995 GCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTCTGTGAATTGAATATT 2054
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QY 1926 GCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTCTGTGAATTGAATATT 1985
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QY 2055 ATTCCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTCAGTTTTG 2114
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QY 1986 ATTCCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTCAGTTTTG 2045
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QY 2046 ATATTTCTAGCTTATCTACTTCCAAACTAATTTTTTATTTTTTGTGCTGAGACTAATCTTATTC 2105
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QY 2175 ATTTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAAACATACCTAAGAAGTA 2234
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QY 2106 ATTTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAAACATACCTAAGAAGTA 2165
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QY 2235 CATTTGTACCTCTATATACCAAAAGCACATTTTAAAAGTGCCATTAAACAAATGTATCACTA 2294
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QY 2166 CATTTGTACCTCTATATACCAAAAGCACATTTTAAAAGTGCCATTAAACAAATGTATCACTA 2225
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QY 2295 GCCCTCCTTTTTCACAAAGAGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATT 2354
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QY 2226 GCCCTCCTTTTTCACAAAGAGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATT 2285
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QY 2286 AAAGCATTTAGAAA 2300
Db |||||||
RESULT 7
US-09-232-160-13
; Sequence 13, Application US/092322160
; Patent No. 6368794
; GENERAL INFORMATION:
; APPLICANT: Steve Daniel
; APPLICANT: James Gilmore
; APPLICANT: Susan G. Stuart
; APPLICANT: Laura Stuve
; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: PA-0003 US
; CURRENT APPLICATION NUMBER: US/09/232,160
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 2029
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 3044710
US-09-232-160-13
Query Match 84.1%; Score 1994; DB 4; Length 2029;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTAGCCCTCAACATA 60
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QY 24 AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTAGCCCTCAACATA 83
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QY 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
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QY 84 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 143
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QY 144 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 203
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QY 181 GTGTTGCTTCTCATTCCATCTGGACCACGAGSCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
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QY 204 GTGTTGCTTCTCATTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 263
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QY 241 GAAGAGCTTTCCATCCAGGTGTCTGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAG 300
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QY 264 GAAGAGCTTTCCATCCAGGTGTCTGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAG 323
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QY 301 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGAGGCCCTGTAGGCTGCTGGGACTAAGT 360
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QY 324 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGAGGCCCTGTAGGCTGCTGGGACTAAGT 383
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QY 361 TTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTGAAACTTTGCAGCTAT 420
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QY 384 TTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTGAAACTTTGCAGCTAT 443
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QY 421 GGCTGGGTGGAGATGGATTCTGTGGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGG 480
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Db 444 GGCTGGGTGGAGATGGATTCTGTGGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGG 503
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Db 504 AAAAAATGGGTGGGTGTCTGTGATTGTGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 563
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Db 564 TGTTACAACCTCATCTGATACCTTGGACTAACTCGTGCATTCAGAAATATATCAACCACAAA 623
QY 601 GATCCCATATTCAAACACTCAAACTGCAACACAAACAAACAGAAATTTATGTCAGTGACAGT 660
Db 624 GATCCCATATTCAAACACTCAAACTGCAACACAAACAAACAGAAATTTATTTGTCAGTGACAGT 683
QY 661 ACCTACTCGGTGGCATCCCTTTACTCTACAATACCTGCCCTACTACTACTCCTCTGCT 720
Db 684 ACCTACTCGGTGGCATCCCTTTACTCTACAATACCTGCCCTACTACTACTCCTCTGCT 743
QY 721 CCAGCTTCACCTCTATTCCACGGAGAAAAAATTGATTTGTGTCACAGAAATTTTATG 780
Db 744 CCAGCTTCACCTCTATTCCACGGAGAAAAAATTGATTTGTGTCACAGAAATTTTATG 803
QY 781 GAAACTAGCACCATGTCTACAGAAACTGAACCAATTTGTTGAAAAATAAAGCAGCATTTCAAG 840
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QY 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTCTGCTCCTCTTC 900
Db 864 AATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTCTGCTCCTCTTC 923
QY 901 TTTGGTGTGCAGCTGGTCTTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCTTCCT 960
Db 924 TTTGGTGTGCAGCTGGTCTTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCTTCCT 983
QY 961 TTTACAAACAAGATCAGCAGAAGGAATGATCGAAACCAAGTAGTAAAGGAGGAGAAG 1020
Db 984 TTTACRAACAAGATCAGCAGAAGGAATGATCGAAACCAAGTAGTAAAGGAGGAGAAG 1043
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Db 1044 GCCAATGATAGCAACCTTAATGAGGAATCAAAGAAACTGATAAAAAACCCAGAAAGTCC 1103
QY 1081 AAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAGTGAAAGTTTAGATGAGACAGAAA 1140
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QY 1141 TGAGGAGACACACCTGAGGTGGTTTCTTTTCATGCTCCTTACCTGCCCTGCCAGCTGGGGAA 1200
Db 1164 TGAGGAGACACACCTGAGGTGGTTTCTTTTCATGCTCCTTACCTGCCCTGCCAGCTGGGGAA 1223
QY 1201 ATCAAAAGGCCAAAGAACCAAGAGAAAGTCCACCCCTGGTTCCTAACTGGAATCAGC 1260
Db 1224 ATCAAAAGGCCAAAGAACCAAGAGAAAGTCCACCCCTGGTTCCTAACTGGAATCAGC 1283
QY 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1320
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QY 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGGCAGCTCAGACCCCTTCTTCA 1560

Db 1524 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGGCAGCTCAGACCCCTTCTTCA 1583
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Db 1584 GCTCTGAAAGAGAAAAACAGTATCCCACTGACATGTCTTCTGAGCCCGGTAAGAGCAAA 1643
QY 1621 AGAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCTATAACTTGAGACCTAA 1680
Db 1644 AGAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCTATAACTTGAGACCTAA 1703
QY 1681 TCTCTGTAAAGCTAAAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1740
Db 1704 TCTCTGTAAAGCTAAAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1763
QY 1741 GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAAT 1800
Db 1764 GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAAT 1823
QY 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACCTGCTGATATTTTCTCT 1860
Db 1824 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACCTGCTGATATTTTCTCT 1883
QY 1861 AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTTTATAAATTTCTATTTTATCT 1920
Db 1884 AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTTTATAAATTTCTATTTTATCT 1943
QY 1921 GAGTTACAGAAATGATTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
Db 1944 GAGTTACAGAAATGATTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 2003
QY 1981 TTCAACAAACATTTGCTGAATA 2002
Db 2004 TTCAACAAACATTTAAAAAAA 2025

RESULT 8

US-09-724-864-28
; Sequence 28, Application US/09724864
; Patent No. 6380362

; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050UI
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 28
; LENGTH: 1896
; TYPE: DNA
; ORGANISM: Mouse

US-09-724-864-28

Query Match 25.4%; Score 603.6; DB 4; Length 1896;
Best Local Similarity 76.2%; Pred. No. 2.3e-162;
Matches 786; Conservative 0; Mismatches 234; Indels 12; Gaps 3;

QY 140 GCTCTGAAGGGTAGGCACCATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCA 199
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Db 42 GCCCCGGAGGGATCTGCACAATGCTCCAGCACACATAGCTGTGTACTCCTCGCCTCTA 101
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Db 102 TTGGACCACTAGGCACCCAGTCCAAGGTGCCGACCTCGTCAAGACCTTTTCCAT---TT 158
QY 260 TGTTCATGCAGAATTATGGGATCACCCCTTGTGAGCAAAAAGCGCAACCCAGCAGCTGAATT 319
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Db 159 CTACATGCAGAATCATGGGCGTTGCCCTTGTGGGCAGAAAACAAAAACCCACAGATGAATT 218

QY	320	TCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAG	379
Db	219	TCACAGAAGCCAAACGAGGCCTGTAAAGATGCTGGGACTGACTCTGCGCAGCAGGACCCAGG	278
QY	380	TTGAAACAGCCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGAT	439
Db	279	TAGAGTCAGCGCAGAAAATCTGGCTTTGAGACTTGCAGCTATGGAATGGGTTGGAGAACAGT	338
QY	440	TCGTGGTCACTCTTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTGGGTGTCC	499
Db	339	TCCTGTGTCATCCCTCGGATTTTCTCAAACCCCCAGGTGTGGGAAGAATGGCAAAGGTGTCC	398
QY	500	TGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATA	559
Db	399	TGATTTGGAATGCTCCCTCCAGCCAAAAGTTCAAAGCCTATTGCCACAACTCATCCGACA	458
QY	560	CTTGGACTAACTCGTGCAATCCAGAAAATTATCACCCACCAAGATCCCATATTCAACACACTC	619
Db	459	CCTGGGTTAACTCCTGCAATCCAGAAAATCGTTACCACATTTTACCCCGTGTGGACACTC	518
QY	620	AAACTGCAACACAAAACAAGAAATTTATGTGAGTGACAGTACCTACTCGGTGGCATCCC	679
Db	519	A-----AACACCCCGCAACAGAGTTTCTGTGAGCAGCAGCGCCTACTTGGCTTCATCCC	572
QY	680	CTTACTCTACAAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTTC	739
Db	573	CTGACTCCACAACACCTG---TTTCTGCCACCACCCCGGGCTCCACCTTTGACCTCCATGG	629
QY	740	CACGGAGAAAAAATTGATTTGTGTACAGAAAGTTTTTATCGAAAACTAGCACCATGTCTA	799
Db	630	CACGGAAGACAAAAAGATTGTATCAGGAAGTTTATACAGAACTTATCACCATGGCTA	689
QY	800	CAGAAACTGAACCATTTGTTGAAAAATAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTG	859
Db	690	CAGAAAACAGAAAGCATTTGTGCAAGTGGAGCAGCATTCAGAAACGAAGCAGCTGGGTTTG	749
QY	860	GAGGTGTCCCCACGGCTGTGCTAGTGTGCTCTCCTCTCTTCTTGGTGTGCAGCTGTGC	919
Db	750	GAGGTGTCCCCACCGCCCTGCTGGTGTGGCTCTCCTCTCTTCTTGGTGTGCGGCTGTGC	809
QY	920	TTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCCCTTCCCTTTTACAAAACAAGATCAGC	979
Db	810	TGGCTGTTTGCTACGTGAAAAGGTATGTGAAGGCCCTTCCCTTTTCACAAACCAAGATCAAC	869
QY	980	AGAAGGAAATGATCGAAACCAAAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTA	1039
Db	870	AGAAGGAAATGATCGAAACCAAGGTTGTAAGGAAGAGAAGGCTGATGACGTCAACGCTA	929
QY	1040	ATGAGGAATCAAAGAAAACTGATAAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTA	1099
Db	930	ATGAAGAATCAAAGAAAAACCATTAATAAACCCAGAGAGGCCAAGAGTCCAACCAAAACTA	989
QY	1100	CCGTGCGATGCCTGGAAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGG	1159
Db	990	CGGTGCGATGCTTAGAAGCTGAAGTTTAGATGCAAGAGAGTGGAGAAGGTGCACACGAGG	1049
QY	1160	CTGGTTTTCTTTC	1171
Db	1050	CAAGTTTTCATGC	1061

RESULT 9

US-08-892-880-11/c
; Sequence 11, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, RETNER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FILING DATE: HERewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,762
FILING DATE: 15-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0490001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

Query Match 14.1%; Score 334; DB 2; Length 339;
Best Local Similarity 98.5%;
Pred. No. 1.1e-85;
Matches 334; Conservative 0; Mismatches 5; Indels

QY	1466	CCTCCTGGCTGCTGAGGCTAGGTGGTTGAAAGCCCAAGGAGTCACTGAGACCAAGGCTT	1522
Db	339	CCTCCTGGCTGCTGAGGCTAGGTGGTTGAAAGCNAAGGAGTCACTGAGACCAAGGCTT	280
QY	1526	TCTCTACTGATTCGCGCAGCTCAGACCCCTTTCTTCAGCTCTGAAAGAGAAACACGTATCCC	1585
Db	279	NCTCTACTGATTCGCGCAGCTCAGACCCCTTNCCTTCAGCTCTGAAAGAGAAACACGTATCCC	220
QY	1586	ACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCCCT	1645
Db	219	ACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCCCT	160
QY	1646	GAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAGCTTAAATAAAGAAA	1705
Db	159	GAAAGCCATGGAGANTCTCATAACTTGAGACCTAATCTCTGTAAGCTTAAATAAAGAAA	100
QY	1706	TAGAACCAAGGCTGAGGATACGACAGTACACTGTGAGCAGGGACTGTAAACACAGACAGGG	1765
Db	99	TAGAACCAAGGCTGAGGATACGACAGTACACTGTGAGCAGGGACTGTAAACACAGACAGGG	40
QY	1766	TCAAAGTGTTTTCTCTGAACACATTGAGTTGGAATCACT	1804
Db	39	TCAAAGTGTTTTCTCTGAACACATTGAGTTGGAATCACT	1

RESULT 10

US-08-892-880-12
 ; Sequence 12, Application US/08892880
 ; Patent No. 5942417
 ; GENERAL INFORMATION:
 ; APPLICANT: NI, JIAN
 ; APPLICANT: GENTZ, REINER L.
 ; APPLICANT: DILLON, PATRICK J.
 ; TITLE OF INVENTION: CD44-LIKE PROTEIN
 ; NUMBER OF SEQUENCES: 15

QY 1675 ACCTAATCTCTGTAAAGCTAAATAAGAAATAGAACAAAGGCTGAGGATACGACAGTAC 1733
|
Db 61 ACCTAATCTCTGTAAAGCTAAATAAGAAATAGAACAAAGGCTGAGGATACGACAGTAC 3
|
RESULT 13
US-09-433-826B-324/c
; Sequence 324, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 324
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-324

Query Match 10.1%; Score 239; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1495 GAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTT 1554
|
Db 241 GAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTT 182
|
QY 1555 TCTTCAGCTCTGAAAGAGAAACACGTCATCCACCTGACATGTCCTTCTGAGCCCGGTAAG 1614
|
Db 181 TCTTCAGCTCTGAAAGAGAAACACGTCATCCACCTGACATGTCCTTCTGAGCCCGGTAAG 122
|
QY 1615 AGCAAAAGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCCATGGAGATTCTCATAACTTGAG 1674
|
Db 121 AGCAAAAGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCCATGGAGATTCTCATAACTTGAG 62
|
QY 1675 ACCTAATCTCTGTAAAGCTAAATAAGAAATAGAACAAAGGCTGAGGATACGACAGTAC 1733
|
Db 61 ACCTAATCTCTGTAAAGCTAAATAAGAAATAGAACAAAGGCTGAGGATACGACAGTAC 3
|

RESULT 14
US-09-604-287A-324/c
; Sequence 324, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 324
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-324

Query Match 10.1%; Score 239; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1495 GAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTT 1554
|
Db 241 GAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTT 182
|
QY 1555 TCTTCAGCTCTGAAAGAGAAACACGTCATCCACCTGACATGTCCTTCTGAGCCCGGTAAG 1614
|
Db 181 TCTTCAGCTCTGAAAGAGAAACACGTCATCCACCTGACATGTCCTTCTGAGCCCGGTAAG 122
|
QY 1615 AGCAAAAGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCCATGGAGATTCTCATAACTTGAG 1674
|
Db 121 AGCAAAAGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCCATGGAGATTCTCATAACTTGAG 62
|
QY 1675 ACCTAATCTCTGTAAAGCTAAATAAGAAATAGAACAAAGGCTGAGGATACGACAGTAC 1733
|
Db 61 ACCTAATCTCTGTAAAGCTAAATAAGAAATAGAACAAAGGCTGAGGATACGACAGTAC 3
|

RESULT 15
US-09-834-759-324/c
; Sequence 324, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 324
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-324

Query Match 10.1%; Score 239; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1495 GAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTT 1554
|
Db 241 GAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTT 182
|
QY 1555 TCTTCAGCTCTGAAAGAGAAACACGTCATCCACCTGACATGTCCTTCTGAGCCCGGTAAG 1614
|
Db 181 TCTTCAGCTCTGAAAGAGAAACACGTCATCCACCTGACATGTCCTTCTGAGCCCGGTAAG 122
|
QY 1615 AGCAAAAGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCCATGGAGATTCTCATAACTTGAG 1674
|
Db 121 AGCAAAAGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCCATGGAGATTCTCATAACTTGAG 62
|
QY 1675 ACCTAATCTCTGTAAAGCTAAATAAGAAATAGAACAAAGGCTGAGGATACGACAGTAC 1733
|
Db 61 ACCTAATCTCTGTAAAGCTAAATAAGAAATAGAACAAAGGCTGAGGATACGACAGTAC 3
|

Search completed: August 16, 2004, 17:08:30
Job time : 176 secs

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OM nucleic - nucleic search, using sw model

Run on: August 16, 2004, 08:16:11 ; Search time 9272 Seconds
(without alignments)
11088.188 Million cell updates/sec

Title: US-10-063-670-5
Perfect score: 2372
Sequence: 1 agcagggaatccggatgtc.....ttaaagcatttagaaaactt 2372

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- GenEmbl:*
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2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
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8: gb_pl:*
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34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2372	100.0	2372	6	AR410761	AR410761 Sequence
2	2372	100.0	2372	6	AX092274	AX092274 Sequence
3	2372	100.0	2372	6	AX454446	AX454446 Sequence
4	2372	100.0	2372	6	AX490924	AX490924 Sequence
5	2372	100.0	2372	6	AX697609	AX697609 Sequence
6	2372	100.0	2372	6	BD075532	BD075532 Secretary
7	2372	100.0	2372	6	BD172392	BD172392 Secreted
8	2372	100.0	2372	6	BD172711	BD172711 Secreted
9	2372	100.0	2372	6	BD173030	BD173030 Secreted
10	2372	100.0	2372	6	BD173349	BD173349 Secreted
11	2372	100.0	2372	6	BD175383	BD175383 Secretary
12	2372	100.0	2372	9	AY358925	AY358925 Homo sapi
13	2282.2	96.2	2313	9	AF118108	AF118108 Homo sapi
14	2245.4	94.7	2282	9	BC026231	BC026231 Homo sapi
15	1994	84.1	2029	6	AR204700	AR204700 Sequence
16	1994	84.1	2029	6	BD222718	BD222718 Human sig
17	1712.4	72.2	1755	6	AX136227	AX136227 Sequence
18	1712.4	72.2	1755	6	BD123566	BD123566 Secretary
19	1712.4	72.2	1755	9	AK075443	AK075443 Homo sapi
20	1437.2	60.6	165698	9	AC009532	AC009532 Homo sapi
21	1191.4	50.2	1285	9	AF127670	AF127670 Homo sapi
22	927.2	39.1	1613	4	AY372937	AY372937 Bos tauru
23	631.8	26.6	716	6	AX136529	AX136529 Sequence
24	631.8	26.6	716	6	BD123769	BD123769 Secretary
25	631	26.6	2027	10	BC038653	BC038653 Mus muscu
26	631	26.6	2027	10	BC038892	BC038892 Mus muscu
27	616.4	26.0	1516	10	MMU311501	AJ311501 Mus muscu
28	500.2	21.1	516	6	AX331191	AX331191 Sequence
29	500.2	21.1	516	6	AX331600	AX331600 Sequence
30	500.2	21.1	516	6	AX332298	AX332298 Sequence
31	500.2	21.1	516	6	AX333352	AX333352 Sequence
32	500.2	21.1	516	6	AX333777	AX333777 Sequence
33	500.2	21.1	516	6	AX407467	AX407467 Sequence
34	485.8	20.5	506	6	AX156239	AX156239 Sequence
35	458.8	19.3	591	6	AX136672	AX136672 Sequence
36	458.8	19.3	591	6	BD123912	BD123912 Secretary
37	450	19.0	451	6	BD076146	BD076146 5' EST of
38	386.2	16.3	603	4	AY304537	AY304537 Sus scrof
39	343	14.5	363	6	BD077623	BD077623 5'EST of
40	331.8	14.0	373	6	BD073800	BD073800 5'EST of
41	246.4	10.4	250	11	GI4689	GI4689 SHGC-13369
42	239	10.1	241	6	AR280816	AR280816 Sequence
43	239	10.1	241	6	AR283312	AR283312 Sequence
44	239	10.1	241	6	AR344080	AR344080 Sequence
45	239	10.1	241	6	AR351281	AR351281 Sequence

ALIGNMENTS

RESULT 1	AR410761	2372 bp	DNA	linear	PAT 18-DEC-2003
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LOCUS	AR410761	2372 bp	DNA	linear	PAT 18-DEC-2003
DEFINITION	Sequence 200 from patent US 6635468.				
ACCESSION	AR410761				
VERSION	AR410761.1	GI:40162261			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 2372)				
AUTHORS	Ashkenazi,A., Botstein,D., Desnoyers,L., Baton,D.L., Ferrara,N., Filvaroff,E., Fong,S., Gao,W.-Q., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J., Kljavina,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A.,				

Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I. Secreted and transmembrane polypeptides and nucleic acids encoding the same JOURNAL Patent: US 6635468-A 200 21-OCT-2003; FEATURES Location/Qualifiers source 1..2372 /organism="unknown" /mol_type="genomic DNA"									
ORIGIN									
Query Match 100.0%; Score 2372; DB 6; Length 2372; Best Local Similarity 100.0%; Pred. No. 0; Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	AGCAGGGAAATCCGGATGTC	CGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA	60					
Db	1	AGCAGGGAAATCCGGATGTC	CGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA	60					
QY	61	GTTCCAGAACTCTCCATCCG	ACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGC	120					
Db	61	GTTCCAGAACTCTCCATCCG	ACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGC	120					
QY	121	CATCTGAGGTGTTTCCCTG	CTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG	180					
Db	121	CATCTGAGGTGTTTCCCTG	CTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG	180					
QY	181	GTGTTGCTTCTCACTTCCA	TCTGACATCTGGACCAAGGCTCCTGGTCCAAGGCTCTTTGGCGTCA	240					
Db	181	GTGTTGCTTCTCACTTCCA	TCTGACATCTGGACCAAGGCTCCTGGTCCAAGGCTCTTTGGCGTCA	240					
QY	241	GAAGAGCTTTCATCCAGGT	GTCAATGAGCAATTAAGGGATCACCCCTTGTGAGCAAAAAG	300					
Db	241	GAAGAGCTTTCATCCAGGT	GTCAATGAGCAATTAAGGGATCACCCCTTGTGAGCAAAAAG	300					
QY	301	GCGAACCAAGCAGCTGAAT	TTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGT	360					
Db	301	GCGAACCAAGCAGCTGAAT	TTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGT	360					
QY	361	TTGGCCGGCAAGGACCAAG	TTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	420					
Db	361	TTGGCCGGCAAGGACCAAG	TTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	420					
QY	421	GGCTGGGTTGGAGATGGAT	TCGTGGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGG	480					
Db	421	GGCTGGGTTGGAGATGGAT	TCGTGGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGG	480					
QY	481	AAAAATGGGTTGGGTGTC	TCTGATTTGGAAAGTTCAGTGAGCCGACAGTTTGCAGCCTAT	540					
Db	481	AAAAATGGGTTGGGTGTC	TCTGATTTGGAAAGTTCAGTGAGCCGACAGTTTGCAGCCTAT	540					
QY	541	TGTTACAACCTCACTCAAA	CTGAACTGCAACACAAACAAAGAAATTTATGTCAGTGACAGT	600					
Db	541	TGTTACAACCTCACTCAAA	CTGAACTGCAACACAAACAAAGAAATTTATGTCAGTGACAGT	600					
QY	601	GATCCCATATTTCAACACT	CAAACTGCAACACAAACAAAGAAATTTATGTCAGTGACAGT	660					
Db	601	GATCCCATATTTCAACACT	CAAACTGCAACACAAACAAAGAAATTTATGTCAGTGACAGT	660					
QY	661	ACCTACTCGGTGGCATCCC	CTTACTCTACAATACCTGCCCTACTACTCTCCTCTGCT	720					
Db	661	ACCTACTCGGTGGCATCCC	CTTACTCTACAATACCTGCCCTACTACTCTCCTCTGCT	720					
QY	721	CCAGCTTCCACTTCTATTCC	ACGGAGAAAAAATTTGATTGTGTACAGAAATTTTATG	780					
Db	721	CCAGCTTCCACTTCTATTCC	ACGGAGAAAAAATTTGATTGTGTACAGAAATTTTATG	780					
QY	781	GAACCTAGCACCATGTCTAC	AGAACTGAACCATTTGTTGAAATTAAGCAGCATTTCAAG	840					
Db	781	GAACCTAGCACCATGTCTAC	AGAACTGAACCATTTGTTGAAATTAAGCAGCATTTCAAG	840					
QY	841	AATGAAGCTGCTGGGTTTG	GAGGTGTCACAGGGCTCTGTAGTGTGCTCTCCTCTTC	900					
Db	841	AATGAAGCTGCTGGGTTTG	GAGGTGTCACAGGGCTCTGTAGTGTGCTCTCCTCTTC	900					

QY	901	TTTGGTGTCTGCAGCTGGT	CTTGGATTTTGGTATGTCAAAAGGTATGTGAAGCCTTCCCT	960					
Db	901	TTTGGTGTCTGCAGCTGGT	CTTGGATTTTGGTATGTCAAAAGGTATGTGAAGCCTTCCCT	960					
QY	961	TTTACAAAACAAGAAATCAG	CAGAAGAAATGATCGAAACCCAAAGTAGTAAAGGAGAGAAG	1020					
Db	961	TTTACAAAACAAGAAATCAG	CAGAAGAAATGATCGAAACCCAAAGTAGTAAAGGAGAGAAG	1020					
QY	1021	GCCAATGATAGCAACCTAAT	GAAGAAATCAAGAAACCCAGAAAGAGTCC	1080					
Db	1021	GCCAATGATAGCAACCTAAT	GAAGAAATCAAGAAACCCAGAAAGAGTCC	1080					
QY	1081	AAGAGTCCAAGCAAAACTAC	CGTGCGATGCCCTGGAAGCTTGAAGTGTAGATGAGACAGAAA	1140					
Db	1081	AAGAGTCCAAGCAAAACTAC	CGTGCGATGCCCTGGAAGCTTGAAGTGTAGATGAGACAGAAA	1140					
QY	1141	TGAGGAGACACACCTGAGS	CTGGTTCTTTTCATGCTCCTTACCTGCCCCAGCTGGGAA	1200					
Db	1141	TGAGGAGACACACCTGAGS	CTGGTTCTTTTCATGCTCCTTACCTGCCCCAGCTGGGAA	1200					
QY	1201	ATCAAAAGGGCCAAAGAAC	CAAGAAAGTCCACCTTGGTTCCCTAACTGGAATCAGC	1260					
Db	1201	ATCAAAAGGGCCAAAGAAC	CAAGAAAGTCCACCTTGGTTCCCTAACTGGAATCAGC	1260					
QY	1261	TCAGGACTGCCATTGGACTA	TGGAGTGCACCAAGAGAATGCCCTTCTCCTTATTGTAAC	1320					
Db	1261	TCAGGACTGCCATTGGACTA	TGGAGTGCACCAAGAGAATGCCCTTCTCCTTATTGTAAC	1320					
QY	1321	CCTGTCTGGATCCTATCCT	ACCTCCAAGCTTCCACGGCCTTCTAGCCTGGCTAT	1380					
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RESULT 3
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LOCUS      2372 bp          DNA          linear          PAT 06-JUL-2002
DEFINITION      Sequence 31 from Patent WO0208284.
ACCESSION      AX454446
VERSION        AX454446.1  GI:21713847
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
AUTHORS      Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
TITLE        Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL      Patent: WO 0208284-A 31 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)
FEATURES      Location/Qualifiers
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source

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ORIGIN

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Best Local Similarity	100.0%;	Pred. No. 0;		
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QY	121	CATCTGAGTGTTCCTGGCT	CTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG	180
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AX490924

LOCUS AX490924 Sequence 31 from Patent WO0200690. DNA linear PAT 16-AUG-2002
DEFINITION AX490924
ACCESSION AX490924
VERSION AX490924.1 GI:22323799

KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1

REFERENCE
AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.

TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis

JOURNAL Patent: WO 0200690-A 31 03 -JAN-2002;
Genentech, Inc. (US)

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QY	181	GTGTTGCTTCTCACTTCC	ATCTGGACACGAGGCTCCTGGTCCAAGGCTCTTTGCCGTGA 240
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DEFINITION Sequence 200 from Patent WO0104311.
ACCESSION AX697609
VERSION AX697609.1 GI:29498705
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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AUTHORS Ashkenazi,A.J., Botstein,D., Desnovers,L., Eaton,D.L., Ferrara,N.,
Filvaroff,E., Fong,S., Gao,W.Q., Gerber,H., Gerritsen,M.E.,
Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Hillan,K.J.,
Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A.,
Stewart,T.A., Tamas,D., Williams,P.M. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0104311-A 200 18-JAN-2001;
Genentech Inc. (US)
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BD075532

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BD075532

2372 bp

DNA

linear

PAT 27-AUG-2002

Secretory and transmembrane polypeptide and nucleic acid encoding the same.

BD075532

GI:22621135

JP 2001516580-A/165

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2372)

Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J.

Secretory and transmembrane polypeptide and nucleic acid encoding the same

Patent: JP 2001516580-A 165 02-OCT-2001; GENENTECH INC

OS Homo sapiens (human)

PN JP 2001516580-A/165

PD 02-OCT-2001

PF 16-SEP-1998

JP 2000511867

PR 17-SEP-1997

US 60/059115,17-SEP-1997

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US 60/066770

PR 24-NOV-1997

US 60/066511,24-NOV-1997

US 60/066453

PR 25-NOV-1997

US 60/066840

PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDLEY GODDARD,DIANE PENICA, PI JEAN CHEN, JEAN YUAN

PI C12N15/09,C07K14/47,C07K14/705,C07K16/18,C07K16/28,C07K19/00,C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/02,/(C12P21/08, PC C12R1:91), C12N15/00,C12N5/00

CC Secretory and transmembrane polypeptide and nucleic acid encoding the same

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BD172392
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VERSION
BD172392.1 GI:28413692
KEYWORDS
JP 2002223786-A/165.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2372)
AUTHORS
Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL
Patent: JP 2002223786-A 165 13-AUG-2002;
GENENTECH INC
COMMENT
OS Homo sapiens (human)
PN JP 2002223786-A/165
PD 13-AUG-2002
PF 18-DEC-2001 JP 2001385135
PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR
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07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR
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24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR
24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR
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WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
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PI JEAN YUAN
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encoding the same
FH Key Location/Qualifiers
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BD172711

LOCUS

DEFINITION

BD172711 2372 bp DNA linear PAT 18-FEB-2003

Secreted and transmembrane polypeptides and nucleic acids encoding the same.

BD172711

ACCESSION

BD172711.1 GI:28414015

VERSION

JP 2002238586-A/165.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 2372)

AUTHORS

Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.

TITLE

Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL

Patent: JP 2002238586-A 165 27-AUG-2002;

COMMENT

GENENTECH INC

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PN JP 2002238586-A/165

PD 27-AUG-2002

PF 18-DEC-2001 JP 2001385205

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WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI		
JIAN ZHENG,		
PI	JEAN YUAN	
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BD173030

LOCUS BD173030 2372 bp DNA linear PAT 18-FEB-2003

DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding the same.

ACCESSION BD173030

VERSION BD173030.1 GI:28414336

KEYWORDS JP 2002238587-A/165.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2372)

AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: JP 2002238587-A 165 27-AUG-2002; GENENTECH INC

COMMENT OS Homo sapiens (human)

PN JP 2002238587-A/165

PD 27-AUG-2002

PF 18-DEC-2001 JP 2001385248

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PH Key Location/Qualifiers

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RESULT 10
BD173349

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

BD173349 2372 bp DNA linear PAT 18-FEB-2003
Secreted and transmembrane polypeptides and nucleic acids encoding the same.

BD173349
BD173349.1 GI:28414660
JP 2002238588-A/165.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2372)

Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and

Yuan,J.

Secreted and transmembrane polypeptides and nucleic acids encoding

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JIAN ZHENG,										
PI	JEAN YUAN									
PC	C12N15/09, C07K14/435, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC									
C12N5/10,										
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RESULT 11
BD175383
LOCUS BD175383 2372 bp DNA linear PAT 18-MAR-2003

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Secretory and transmembrane polypeptide and nucleic acid encoding the same.
BD175383
JP 2002253280-A/165.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2372)
Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.
Secretory and transmembrane polypeptide and nucleic acid encoding the same
Patent: JP 2002253280-A 165 10-SEP-2002;
GENENTECH INC
OS Homo sapiens (human)
PN JP 2002253280-A/165
PD 10-SEP-2002
PF 18-DEC-2001 JP 2001385319
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ACCESSION AY358925
VERSION AY358925.1 GI:37182967
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.

TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 2372)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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ORIGIN
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION LYVE-1 mRNA, complete cds.
ACCESSION AF118108
VERSION AF118108.1 GI:5359672
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2313)
AUTHORS Banerji,S., Ni,J., Wang,S.X., Clasper,S., Su,J., Tammi,R., Jones,M.
and Jackson,D.G.
TITLE LYVE-1, a new homologue of the CD44 glycoprotein, is a
lymph-specific receptor for hyaluronan
J. Cell Biol. 144 (4), 789-801 (1999)
99156989
10037799
REFERENCE 2 (bases 1 to 2313)
AUTHORS Jackson,D.G., Banerji,S. and Ni,J.
TITLE Direct Submission
JOURNAL Submitted (06-JAN-1999) MRC Human Immunology Unit, Univ. of Oxford,
John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK
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ORIGIN

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AR204700
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DEFINITION Sequence 13 from patent US 6368794.
ACCESSION AR204700
VERSION AR204700.1 GI:21502094
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2029)
TITLE Daniel,S., Gilmore,J., Stuart,S.G. and Stuve,L.L.
Detection of altered expression of genes regulating cell proliferation
JOURNAL Patent: US 6368794-A 13 09-APR-2002;
FEATURES Location/Qualifiers
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ORIGIN

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Best local Similarity 99.8%; Pred. No. 0;
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Search completed: August 16, 2004, 15:24:08
Job time : 9282 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 16:57:05 ; Search time 880 Seconds
(without alignments)
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Perfect score: 2372
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Scoring table: IDENTITY_NUC
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Searched: 3373863 seqs, 2124099041 residues 6747726
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Minimum DB seq length: 0
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Listing first 800 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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c 105	500.2	21.1	516	6	ABL63363	Ab163363 Breast ca	c 178	51	2.2	20579	6	ABQ67074	Abq67074 Human ang
c 106	500.2	21.1	516	6	ABL63772	Ab163772 Breast ca	c 179	50.8	2.1	5407	6	ABL34090	Ab134090 Human imm
c 107	500.2	21.1	516	6	ABL65524	Ab165524 Lung canc	c 180	50.6	2.1	392	7	ABX39643	Abx39643 Bovine ES
c 108	500.2	21.1	516	6	ABN93616	Abn93616 Gene #114	c 181	50.6	2.1	5504	6	ABL70350	Ab170350 Chemicall
c 109	485.8	20.5	506	4	AAH55571	Aah55571 Human bre	c 182	50.6	2.1	5504	6	AAS61309	Aas61309 Human gen
c 110	458.8	19.3	591	5	AAF94160	Aaf94160 Primer sp	c 183	50.4	2.1	8056	7	ABZ10100	Abz10100 Haematopo
111	450	19.0	451	2	AAX41156	Aax41156 Human sec	c 184	50.4	2.1	12237	6	ABL34358	Ab134358 Human imm
112	440	18.5	486	8	ACH22904	Ach22904 Human adu	185	50	2.1	50	2	AAH52401	Aax52401 Probe use
113	419.4	17.7	472	8	ACH22239	Ach22239 Human adu	186	50	2.1	50	3	ADC78525	Adc78525 Human PRO
114	406	17.1	499	8	ACH30085	Ach30085 Human tes	187	50	2.1	50	4	AAF72559	Aaf72559 Human PRO
115	403	17.0	441	8	ACH17082	Ach17082 Human adu	188	50	2.1	50	7	ACA59064	Aca59064 Human PRO
116	397	16.7	411	8	ACH20895	Ach20895 Human adu	189	50	2.1	50	7	ACA58461	Aca58461 Probe #38
c 117	387.6	16.3	820	10	ADE71448	Ade71448 Dog cdNA	190	50	2.1	50	7	ACA60168	Aca60168 Human sec
118	343	14.5	363	2	AAX51631	Aax51631 Human sec	191	50	2.1	50	7	ACD07568	Acd07568 Novel hum
119	331.8	14.0	373	2	AAX51631	Aax51631 Human sec	192	50	2.1	50	7	ABX71616	Abx71616 Human sec
120	328.6	13.9	559	10	ADE71446	Ade71446 Rat cdNA	193	50	2.1	50	7	ACH06948	Ach06948 Human sec
c 121	239	10.1	241	4	AAF17836	Aaf17836 Human bre	194	50	2.1	50	7	ABX96185	Abx96185 Human sec
c 122	239	10.1	241	4	AAS47266	Aas47266 Human bre	195	50	2.1	50	7	ACA05506	Aca05506 Human sec
c 123	239	10.1	241	6	ABS63867	Abs63867 Human bre	196	50	2.1	50	7	ACD20173	Acd20173 Human sec
c 124	239	10.1	241	7	ABT33079	Abt33079 Human tum	197	50	2.1	50	7	ACA54976	Aca54976 Novel sec
c 125	239	10.1	241	10	ADE44276	Ade44276 Human CDN	198	50	2.1	50	8	ACD19811	Acd19811 Human sec
c 126	238	10.0	308	6	ABL63797	Ab163797 Breast ca	199	50	2.1	50	8	ADB29410	Adb29410 Human sec
c 127	238	10.0	308	6	ABL63384	Ab163384 Breast ca	200	50	2.1	50	8	ADA18266	Ada18266 Human sec
c 128	238	10.0	308	6	ABL63798	Ab163798 Breast ca	201	50	2.1	50	8	ACD66958	Acd66958 Human sec
c 129	238	10.0	308	6	ABN95189	Abn95189 Gene #168	202	50	2.1	50	8	ACD83119	Acd83119 Human PRO
c 130	237	10.0	241	4	AAF17835	Aaf17835 Human bre	203	50	2.1	50	8	ADA16241	Ada16241 Human sec
c 131	237	10.0	241	4	AAS47265	Aas47265 Human bre	204	50	2.1	50	8	ADA42386	Ada42386 Human sec
c 132	237	10.0	241	6	ABS63866	Abs63866 Human bre	205	50	2.1	50	8	ACD23297	Acd23297 Human PRO
c 133	237	10.0	241	7	ABT33078	Abt33078 Human tum	206	50	2.1	50	8	ADA16665	Ada16665 Human sec
c 134	237	10.0	241	10	ADE44275	Ade44275 Human CDN	207	50	2.1	50	8	ADA13094	Ada13094 Human sec
c 135	226.2	9.5	239	6	ABL65603	Ab165603 Lung canc	208	50	2.1	50	8	ADA1962	Ada1962 Human sec
c 136	226.2	9.5	239	6	ABL63605	Ab163605 Breast ca	209	50	2.1	50	8	ADA17309	Ada17309 Human sec
c 137	226.2	9.5	239	6	ABL66203	Ab166203 Lung canc	210	50	2.1	50	8	ADA42812	Ada42812 Human sec
c 138	226.2	9.5	239	6	ABL64015	Ab164015 Breast ca	211	50	2.1	50	8	ACD23659	Acd23659 Human PRO
c 139	226.2	9.5	239	6	ABN94227	Abn94227 Gene #725	212	50	2.1	50	9	ADB77731	Adb77731 Human sec
140	212.2	8.9	279	10	ADE71447	Ade71447 Rat cdNA	213	50	2.1	50	9	ADB74867	Adb74867 Human sec
141	179.2	7.6	469	4	ABA54110	Aba54110 Human foe	214	50	2.1	50	9	ADC28513	Adc28513 Human sec
142	179.2	7.6	469	4	AAI33763	Aai33763 Probe #24	215	50	2.1	50	9	ADC39713	Adc39713 Human sec
143	179.2	7.6	469	4	ABA23859	Aba23859 Probe #23	216	50	2.1	50	9	ADC40227	Adc40227 Human sec
144	179.2	7.6	469	4	AAK27829	Aak27829 Human bon	217	50	2.1	50	9	ADC19051	Adc19051 Human sec
145	179.2	7.6	469	4	ABS27409	Abs27409 Human liv	218	50	2.1	50	9	ADC34351	Adc34351 Human sec
146	179.2	7.6	469	6	ABS02280	Abs02280 Human gen	219	50	2.1	50	9	ADC29406	Adc29406 Human sec
147	175	7.4	457	4	AAI33382	Aai33382 Probe #20	220	50	2.1	50	9	ADC28937	Adc28937 Human sec
148	175	7.4	457	6	ABS01959	Abs01959 Human gen	221	50	2.1	50	9	ADC40822	Adc40822 Human sec
149	129	5.4	141	4	ABA66678	Aba66678 Human foe	222	50	2.1	50	9	ADC19479	Adc19479 Human sec
150	129	5.4	141	4	AAI46891	Aai46891 Probe #15	223	50	2.1	50	9	ADC33927	Adc33927 Human sec
151	129	5.4	141	4	ABA33740	Aba33740 Probe #12	224	50	2.1	50	9	ADC12997	Adc12997 Human sec
152	129	5.4	141	4	AAK40837	Aak40837 Human bon	225	50	2.1	50	9	ADC12449	Adc12449 Human sec
153	129	5.4	141	4	ABS40414	Abs40414 Human liv	226	50	2.1	50	9	ADD05004	Add05004 Human sec
154	129	5.4	141	6	ABS14788	Abs14788 Human gen	227	50	2.1	50	9	ADD04010	Add04010 Human sec
155	106	4.5	106	4	AAI46523	Aai46523 Probe #15	228	50	2.1	50	9	ADD03586	Add03586 Human sec
156	106	4.5	106	6	ABS14478	Abs14478 Human gen	229	50	2.1	50	9	ADE34838	Ade34838 Human sec
157	60	2.5	60	6	ABN38121	Abn38121 Human spl	230	50	2.1	50	10	ADE79283	Ade79283 Human sec
c 158	58.2	2.5	641	6	ABQ56694	Abq56694 Human col	231	50	2.1	50	10	ADE79707	Ade79707 Human sec
c 159	56.8	2.4	8056	7	ABZ10100	Abz10100 Haematopo	232	50	2.1	50	10	ADE73383	Ade73383 Human sec
160	56.6	2.4	2000	7	ADA71938	Ada71938 Rice gene	233	50	2.1	50	10	ADE73918	Ade73918 Human sec
161	56.6	2.4	6216	6	ABK39932	Abk39932 Human che	c 234	49.6	2.1	37515	6	ABQ66998	Abq66998 Human ang
162	56.6	2.4	6216	6	ABL70139	Ab170139 Chemicall	c 235	49.4	2.1	47108	6	ABK31511	Abk31511 Signal tr
163	55.8	2.4	8056	7	ABZ10246	Abz10246 Haematopo	c 236	49.4	2.1	8305	6	ABL33569	Ab133569 Human imm
164	55.4	2.3	339	7	ACC43051	Acc43051 Nucleotid	237	49.4	2.1	47841	6	ABQ80553	Abq80553 Human Can
c 165	55.2	2.3	8056	7	ABZ10246	Abz10246 Haematopo	c 238	49.4	2.1	73334	6	ABL34125	Ab134125 Human imm
c 166	55	2.3	83391	6	ABQ67093	Abq67093 Human ang	c 239	49.4	2.1	73334	6	ABL92319	Ab192319 Chemicall
167	54.2	2.3	11922	3	AAW70187	Aaw70187 Plasmodi	c 240	49.2	2.1	7461	6	ABL33784	Ab133784 Human imm
168	54.2	2.3	15373	6	ABL32467	Ab132467 Human imm	c 241	49.2	2.1	21354	4	AAS46815	Aas46815 Tumour su
c 169	53.8	2.3	11790	6	ABL32542	Ab132542 Human imm	c 242	49.2	2.1	302250	6	ABL67703	Ab167703 Oesophagu

C 243	49	2.1	5430	4	AAS46292	Aas46292 Tumour su
244	49	2.1	6106	4	AAS46429	Aas46429 Tumour su
245	49	2.1	6106	6	ABK40031	Abk40031 Human che
246	49	2.1	6106	6	ABL33472	Abl33472 Human imm
247	49	2.1	15767	6	ABL33207	Ab133207 Human imm
248	49	2.1	15767	6	ABL34553	Ab134553 Human met
C 249	48.8	2.1	9810	6	ABL32426	Abl32426 Human imm
C 250	48.8	2.1	12025	6	ABL33299	Abl33299 Human imm
C 251	48.8	2.1	13202	6	ABL33485	Abl33485 Human imm
252	48.8	2.1	13712	6	ABL33530	Abl33530 Human imm
C 253	48.8	2.1	32392	6	ABL56203	Ab156203 AmEPV gen
254	48.6	2.0	6154	6	ABK31200	Abk31200 Signal tr
255	48.6	2.0	6154	6	ABL70167	Abl70167 Chemicall
256	48.6	2.0	6154	6	AAS61112	Aas61112 Human gen
C 257	48.6	2.0	10749	2	AAX20257	Aax20257 Borrelia
C 258	48.6	2.0	11172	6	ABL34053	Ab134053 Human imm
259	48.6	2.0	17137	6	ABL32191	Ab132191 Human imm
C 260	48.4	2.0	6775	6	ABQ67160	Abq67160 Human ang
261	48.4	2.0	110000	6	ABA92787_3	Continuation (4 of
262	48.2	2.0	972	4	ABA06490	Aba06490 Human cDN
263	48.2	2.0	972	6	ABV83827	Abv83827 Human pol
264	48.2	2.0	1587	2	AAV41923	Aav41923 Nucleotid
265	48.2	2.0	1720	2	AAV34196	Aav34196 Human sec
266	48.2	2.0	1720	7	ACD08067	Acd08067 cDNA enco
267	48.2	2.0	2013	4	AAF29460	Aaf29460 Human TAN
268	48.2	2.0	2013	7	ACD66767	Acd66767 Secreted
269	48.2	2.0	2013	8	ADB90775	Adb90775 Human TAN
270	48.2	2.0	2496	2	AAX20297	Aax20297 Borrelia
271	48.2	2.0	2730	4	AAF29459	Aaf29459 Human TAN
272	48.2	2.0	2730	7	ACD66766	Acd66766 Secreted
273	48.2	2.0	2730	8	ADB90774	Adb90774 Human cDN
274	48.2	2.0	2878	7	AAD48133	Aad48133 Human cho
275	48.2	2.0	3476	4	AAA91017	Aaa91017 Human sec
276	48.2	2.0	3476	6	ABK69986	Abk69986 cDNA enco
277	48.2	2.0	3476	8	ADA01319	Ada01319 Human PRO
278	48.2	2.0	3476	8	ADA43748	Ada43748 Human cDN
279	48.2	2.0	3476	8	ADA43516	Ada43516 Human cDN
280	48.2	2.0	3476	8	ADA01191	Ada01191 Human PRO
281	48.2	2.0	3476	8	ADA01075	Ada01075 Human cDN
282	48.2	2.0	3476	8	ADA43632	Ada43632 Human cDN
283	48.2	2.0	3476	8	ADA06894	Ada06894 Human PRO
284	48.2	2.0	3476	8	ADA08382	Ada08382 Novel hum
285	48.2	2.0	3476	8	ADB99675	Adb99675 Human PRO
286	48.2	2.0	3476	8	ADB86958	Adb86958 Human PRO
287	48.2	2.0	3476	8	ADB66113	Adb66113 Human cDN
288	48.2	2.0	3476	9	ADB99791	Adb99791 Human PRO
289	48.2	2.0	3476	9	ADB99446	Adb99446 Novel hum
290	48.2	2.0	3476	9	ADB65997	Adb65997 Human cDN
291	48.2	2.0	3476	9	ADC23395	Adc23395 Human cDN
292	48.2	2.0	3476	9	ADC26088	Adc26088 Human PRO
293	48.2	2.0	3476	9	ADE04915	Ade04915 Human PRO
294	48.2	2.0	3476	9	ADE11221	Ade11221 Human PRO
295	48.2	2.0	3476	9	ADD88152	Add88152 Human PRO
296	48.2	2.0	3476	9	ADD95447	Add95447 Human cDN
297	48.2	2.0	3476	9	ADE06377	Ade06377 Human PRO
298	48.2	2.0	3476	9	ADE38152	Ade38152 Human PRO
299	48.2	2.0	3476	9	ADD88268	Add88268 Human PRO
300	48.2	2.0	3476	9	ADD90849	Add90849 Human cDN
301	48.2	2.0	3476	10	ADE51702	Ade51702 Human cDN
302	48.2	2.0	3476	10	ADE51818	Ade51818 Human cDN
303	48.2	2.0	3476	10	ADE37676	Ade37676 Human cDN
304	48.2	2.0	3476	10	ADE37560	Ade37560 Human cDN
305	48.2	2.0	3476	10	ADD95331	Add95331 Human cDN
306	48.2	2.0	3476	10	ADE38031	Ade38031 Human PRO
307	48.2	2.0	3476	10	ADE76120	Ade76120 Human PRO
308	48.2	2.0	3476	10	ADE39443	Ade39443 Human PRO
309	48.2	2.0	3476	10	ADE04247	Ade04247 Human PRO
310	48.2	2.0	3476	10	ADE39844	Ade39844 Human PRO
311	48.2	2.0	3476	10	ADE19709	Ade19709 Human PRO
312	48.2	2.0	3476	10	ADE77287	Ade77287 Human cDN
313	48.2	2.0	3476	10	ADE65395	Ade65395 Human PRO
314	48.2	2.0	3476	10	ADE76004	Ade76004 Human PRO
315	48.2	2.0	3476	10	ADE37915	Ade37915 Human PRO

316	48.2	2.0	3476	10	ADE64525	Ade64525 Human PRO
317	48.2	2.0	3476	10	ADE38860	Ade38860 Human PRO
318	48.2	2.0	3476	10	ADE51934	Ade51934 Human cDN
319	48.2	2.0	3476	10	ADD90965	Add90965 Human cDN
320	48.2	2.0	3476	10	ADE38744	Ade38744 Human PRO
321	48.2	2.0	3476	10	ADE37444	Ade37444 Human cDN
322	48.2	2.0	3476	10	ADE06261	Ade06261 Human PRO
323	48.2	2.0	3476	10	ADD90120	Add90120 Human cDN
324	48.2	2.0	3476	10	ADE38628	Ade38628 Human PRO
325	48.2	2.0	3476	10	ADE39559	Ade39559 Human PRO
326	48.2	2.0	3476	10	ADD89164	Add89164 Human PRO
327	48.2	2.0	3476	10	ADD88931	Add88931 Human PRO
328	48.2	2.0	3476	10	ADE19825	Ade19825 Human PRO
329	48.2	2.0	3476	10	ADE77403	Ade77403 Human cDN
330	48.2	2.0	3476	10	ADE65279	Ade65279 Human PRO
331	48.2	2.0	3476	10	ADE39327	Ade39327 Human PRO
332	48.2	2.0	3476	10	ADE38512	Ade38512 Human cDN
C 333	48.2	2.0	5430	4	AAS28917	Aas28917 Human imm
C 334	48.2	2.0	5430	9	ADB31758	Adb31758 Human nov
C 335	48.2	2.0	6106	4	AAS46429	Aas46429 Tumour su
C 336	48.2	2.0	6106	6	ABK40031	Abk40031 Human che
C 337	48.2	2.0	6106	6	ABL333472	Abl33472 Human imm
C 338	48	2.0	5362	6	ABK28414	Abk28414 DNA trans
339	47.8	2.0	47108	6	ABK31511	Abk31511 Signal tr
C 340	47.6	2.0	700	4	AAH93026	Aah93026 Human inf
C 341	47.6	2.0	9965	6	ABL33527	Ab133527 Human imm
342	47.6	2.0	12578	4	AAS46660	Aas46660 Tumour su
343	47.6	2.0	12781	4	AAS46385	Aas46385 Tumour su
344	47.6	2.0	12781	6	ABL92228	Abl92228 Chemicall
345	47.6	2.0	12781	9	ADB54127	Adb54127 Pretreate
346	47.6	2.0	12781	9	ADB54255	Adb54255 Pretreate
347	47.6	2.0	32392	6	ABL56203	Ab156203 AmEPV gen
348	47.4	2.0	40862	6	ABL34073	Ab134073 Human imm
C 349	47.2	2.0	883	4	AAL15210	Aal15210 Human bre
350	47.2	2.0	5413	4	AAS46694	Aas46694 Tumour su
351	47.2	2.0	6074	6	ABK28374	Abk28374 DNA trans
C 352	47.2	2.0	6174	4	AAS46433	Aas46433 Tumour su
353	47.2	2.0	6191	6	ABL33216	Ab133216 Human imm
354	47.2	2.0	6191	6	ABK31306	Abk31306 Signal tr
355	47.2	2.0	6191	6	ABL70281	Ab170281 Chemicall
356	47.2	2.0	6191	6	ABN80160	Abn80160 Human che
C 357	47.2	2.0	7669	6	ABL32628	Ab132628 Human imm
C 358	47.2	2.0	17137	6	ABL32191	Ab132191 Human imm
359	47.2	2.0	17144	4	AAS46665	Aas46665 Tumour su
C 360	47.2	2.0	19236	6	ABN80227	Abn80227 Human che
361	47.2	2.0	110000	5	AAI61373_0	Aai61373 Soybean 3
C 362	47	2.0	4045	4	AAS46740	Aas46740 Tumour su
363	47	2.0	5006	5	AAD22381	Aad22381 Cotton ol
C 364	47	2.0	7057	4	AAS46601	Aas46601 Tumour su
C 365	47	2.0	7057	6	ABL33848	Ab133848 Human imm
C 366	47	2.0	7057	6	ABL34594	Ab134594 Human met
C 367	47	2.0	7057	6	ABL70407	Ab170407 Chemicall
C 368	47	2.0	7057	6	AAS61354	Aas61354 Human gen
C 369	47	2.0	11964	6	ABQ67025	Abq67025 Human ang
C 370	47	2.0	16258	6	ABK40038	Abk40038 Human che
C 371	47	2.0	16258	6	ABL70376	Ab170376 Chemicall
372	46.8	2.0	3153	4	AAF29464	Aaf29464 Murine br
373	46.8	2.0	3153	7	ACD66770	Acd66770 Secreted
374	46.8	2.0	3153	8	ADB90788	Adb90788 Mouse cDN
C 375	46.8	2.0	5987	6	ABL33563	Ab133563 Human imm
C 376	46.8	2.0	5987	6	ABQ67102	Abq67102 Human ang
C 377	46.8	2.0	5987	9	ADB54180	Adb54180 Pretreate
C 378	46.8	2.0	5987	9	ADB54308	Adb54308 Pretreate
C 379	46.8	2.0	6301	6	ABL32052	Ab132052 Human imm
380	46.8	2.0	9760	6	ABK31243	Abk31243 Signal tr
381	46.8	2.0	9760	6	ABL70198	Ab170198 Chemicall
382	46.8	2.0	9760	6	AAS61156	Aas61156 Human gen
C 383	46.8	2.0	12968	4	AAS45494	Aas45494 Chemicall
C 384	46.8	2.0	12968	4	AAS46779	Aas46779 Tumour su
C 385	46.8	2.0	12968	6	ABL34085	Ab134085 Human imm
C 386	46.8	2.0	12968	6	ABK28424	Abk28424 DNA trans
C 387	46.8	2.0	12968	6	ABN80285	Abn80285 Human che
388	46.8	2.0	50000	6	ABL56202	Ab156202 AmEPV gen

389 AAC02796 Human sec
390 AAL15210
391 ADA71938
392 ABN86507
393 ABK63681
394 AAQ14263
395 ABL33248
396 ABL34598
397 ABL70409
398 ABL33964
399 ABL32465
400 ABL33512
401 ABL32298
402 ABL34155
403 ABL34073
404 ABL55643
405 AAH54899
406 ABL32714
407 ABL92301
408 ABL49370
409 ABL70459
410 AAS61424
411 ABL34026
412 AAS46717
413 AAN60472
414 AAS46331
415 ABK28177
416 ABL33763
417 ABL33487
418 ADB54312
419 ADE37779
420 ABL32299
421 ABL5743
422 ABL32396
423 ADB37663
424 ABL55643
425 ABL5218
426 ACA64845
427 AAX99555
428 ABQ67021
429 ABL32430
430 ABL92204
431 ABL49313
432 ABQ67062
433 ABK39994
434 ABL32839
435 ABL31519
436 ABL70606
437 AAS61445
438 ABK31343
439 AAS61238
440 ABL32625
441 ABL33998
442 AAF12929
443 ABL33518
444 ABL32374
445 ABK33931
446 ABL34486
447 ADA20366
448 ADA84173
449 ABL32505
450 ABL32030
451 ABL32493
452 ABL33140
453 ABL32257
454 ABL31207
455 ABK31207
456 ADE54267
457 ADE84189
458 ABL33949
459 AAH51601
460 AAS09301
461 AAX08523

Aac02796 Human sec
Aal15210 Human bre
Ada71938 Rice gene
Abn86507 Rat glyco
Abk63681 Rat seque
Aaq14263 p-meta-1
Abl33248 Human imm
Abl34598 Human met
Abl70409 Chemicall
Abl33964 Human imm
Abl32465 Human imm
Abl33512 Human imm
Abl32298 Human imm
Abl34155 Human imm
Abl34073 Human imm
Abl55643 AmEPV gen
Aah54899 S. epider
Abl32714 Human imm
Abl92301 Chemicall
Abl49370 Human pol
Abl70459 Chemicall
Aas61424 Human gen
Abl34026 Human imm
Aas46717 Tumour su
Aan60472 Sequence
Aas46331 Tumour su
Aak28177 DNA trans
Abl33763 Human imm
Abl33487 Human imm
Adb54312 Pretreat
Ade37779 Human che
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Abk28396 DNA trans
Aas61427 Human gen
Adb37663 Human che
Abl55643 AmEPV gen
Aca64845 Human HNR
Aax99555 Nucleic a
Abq67021 Human ang
Abl32430 Human imm
Abl92204 Chemicall
Abl49313 Human pol
Abq67062 Human ang
Abk39994 Human che
Abl32839 Human imm
Abk31519 Signal tr
Abl70606 Chemicall
Aas61445 Human gen
Abl70304 Chemicall
Aas61238 Human gen
Abl32625 Human imm
Abl33998 Human imm
Aaf12929 Aspergill
Abl33518 Human imm
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Ada84173 Human ren
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Abl32257 Human imm
Abl31207 Signal tr
Abz10177 Haematopo
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Ade84189 Human lym
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Aax08523 NBP46 (ro

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ADC85260
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ABQ9790
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ABL70146

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Aad22328 Chemicall
Aas45315 Chemicall
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Abn80039 Human che
Abl34493 Human met
Abl32917 Human imm
Abl70543 Chemicall
Abl70604 Chemicall
Abq67149 Human ang
Continuation (7 of
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Aaq34622 Cytosolic
Aaq12540 GS3A prom
Abq67043 Human ang
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Adb54184 Pretreat
Ade37769 Human che
Abl34076 Human imm
Abn79996 Human che
Abl32487 Human imm
Aas45393 Chemicall
Abl33295 Human imm
Abk28238 DNA trans
Abl33673 Human imm
Abl32630 Human imm
Abk40018 Human che
Abl32941 Human imm
Abl32766 Human imm
Aax20253 Borrelia
Aaq02047 Sequence
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Abl33161 Human imm
Abl32738 Human imm
Abl54323 Chemicall
Abq67015 Human ang
Abq67074 Human ang
Abl70603 Chemicall
Aas45313 Chemicall
Abk28152 DNA trans
Abk28394 DNA trans
Abl32739 Human imm
Aax20263 Borrelia
Abk40061 Human che
Aas45414 Chemicall
Abk28267 DNA trans
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Abl70502 Chemicall
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ADC85260 Human Ptp
Ada02780 Human PTP
ADB72518 Human PTP
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ABQ9790 Alloiococ
Aaz37082 DNA seque
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ADE84162 Human lym
AAQ24134 50 kD sub
ABZ59722 T. thermo
ABL34102 Human imm
ABL33666 Human imm
ABL32820 Human imm
ABK31185 Signal tr
ABL70146 Chemicall

535	44.4	1.9	6239	6	AAS61072	Aas61072 Human gen
536	44.4	1.9	7168	6	ABL92231	Abl92231 Chemicall
537	44.4	1.9	7168	6	AAD22318	Aad22318 Chemicall
C 538	44.4	1.9	7189	6	ABN80026	Abn80026 Human che
	44.4	1.9	8032	6	ABK31479	Abk31479 Signal tr
C 539	44.4	1.9	8032	6	ABL70448	Abl70448 Chemicall
C 540	44.4	1.9	8032	6	AAS61409	Aas61409 Human gen
C 541	44.4	1.9	8032	6	AAS61356	Abl33568 Human imm
542	44.4	1.9	8305	6	AZ29911	Aaz29911 cDNA enco
C 543	44.4	1.9	8310	2	ABL32668	Ab132668 Human imm
C 544	44.4	1.9	11049	6	ABL92218	Abl92218 Chemicall
C 545	44.4	1.9	11049	6	ABL49321	Ab149321 Human pol
C 546	44.4	1.9	11049	6	AAS46698	Aas46698 Tumour su
547	44.4	1.9	11694	4	AAS46698	Aas46698 Tumour su
C 548	44.4	1.9	16633	6	ABN79985	Abn79985 Human che
C 549	44.4	1.9	18283	6	ABL70501	Abl70501 Chemicall
C 550	44.4	1.9	18283	6	AAS61362	Aas61362 Human gen
C 551	44.4	1.9	34688	6	ABQ67060	Abq67060 Human ang
C 552	44.4	1.9	83391	6	ABQ67094	Abq67094 Human ang
C 553	44.4	1.9	110000	8	ADB12064_09	Continuation (10 o
	44.4	1.9	697	4	AAS28824	Aas28824 Human imm
554	44.2	1.9	697	4	ABA06691	Aba06691 Human cDN
555	44.2	1.9	697	4	ABV84028	Abv84028 Human pol
556	44.2	1.9	697	6	ADB31549	Adb31549 Human cDN
557	44.2	1.9	731	2	AAQ31693	Aaq31693 RsaI rest
C 558	44.2	1.9	1351	2	AAZ17145	Aaz17145 Human gen
	44.2	1.9	2000	6	ABZ17044	Abz17044 Arabidops
560	44.2	1.9	2000	7	ADA69322	Ada69322 Arabidops
561	44.2	1.9	5349	6	ABL32341	Ab132341 Human imm
C 562	44.2	1.9	6012	6	ABK31370	Abk31370 Signal tr
	44.2	1.9	6012	6	ABL70327	Abl70327 Chemicall
564	44.2	1.9	6012	6	AAS61274	Aas61274 Human gen
565	44.2	1.9	6109	6	ABL32326	Ab132326 Human imm
566	44.2	1.9	6109	6	AAS61077	Aas61077 Human gen
567	44.2	1.9	6109	6	ABL32890	Ab132890 Human imm
C 568	44.2	1.9	6131	6	ABK31353	Abk31353 Signal tr
	44.2	1.9	6147	6	ABL33047	Ab133047 Human imm
C 570	44.2	1.9	6290	6	ABL33930	Ab133930 Human imm
C 571	44.2	1.9	7456	6	ABL92292	Abl92292 Chemicall
C 572	44.2	1.9	7456	6	ABL32530	Ab132530 Human imm
C 573	44.2	1.9	7644	6	AAS46435	Aas46435 Tumour su
C 574	44.2	1.9	8093	4	ABK33973	Abk33973 Human DNA
C 575	44.2	1.9	8093	6	ABL92236	Abl92236 Chemicall
C 576	44.2	1.9	8093	6	ABL49331	Ab149331 Human MH
C 577	44.2	1.9	8093	6	ABZ10031	Abz10031 Haematopo
C 578	44.2	1.9	8093	7	ADA20360	Ada20360 Prostate
C 579	44.2	1.9	8093	7	ADA84167	Ada84167 Human ren
C 580	44.2	1.9	8093	7	ADB54139	Adb54139 Pretreate
C 581	44.2	1.9	8093	9	ADE84113	Ade84113 Human lym
C 582	44.2	1.9	8093	9	ABL33068	Ab133068 Human imm
C 583	44.2	1.9	9117	6	AAS45453	Aas45453 Chemicall
	44.2	1.9	9515	4	ABK28308	Abk28308 DNA trans
584	44.2	1.9	9515	6	ABN80245	Abn80245 Human che
585	44.2	1.9	9515	6	ABK28452	Abk28452 DNA trans
586	44.2	1.9	11187	6	ABL70501	Abl70501 Chemicall
587	44.2	1.9	18283	6	AAS61362	Aas61362 Human gen
588	44.2	1.9	18283	6	ABQ67006	Abq67006 Human ang
589	44.2	1.9	33053	6	ABX46069	Abx46069 Bovine ES
C 590	44.2	1.9	419	7	AAS45511	Aas45511 Chemicall
	44	1.9	3007	4	ABK28445	Abk28445 DNA trans
C 591	44	1.9	3007	6	ABQ67144	Abq67144 Human ang
C 592	44	1.9	3151	6	AAD48465	Aad48465 Brassica
C 593	44	1.9	3750	7	ABL32538	Ab132538 Human imm
C 594	44	1.9	5820	6	ABK31237	Abk31237 Signal tr
C 595	44	1.9	6129	6	ABL70538	Ab170538 Chemicall
C 596	44	1.9	6129	6	AAS61150	Aas61150 Human gen
C 597	44	1.9	6129	6	AAS61176	Aas61176 Human gen
C 598	44	1.9	6223	6	AAS45422	Aas45422 Chemicall
C 599	44	1.9	6306	4	ABL33260	Ab133260 Human imm
C 600	44	1.9	6437	6	ABK31424	Abk31424 Signal tr
601	44	1.9	7321	6	ABL70385	Ab170385 Chemicall
C 602	44	1.9	7321	6	AAS61337	Aas61337 Human gen
C 603	44	1.9	7321	6	ABL32914	Ab132914 Human imm
C 604	44	1.9	7522	6	ABL33013	Ab133013 Human imm
C 605	44	1.9	7597	6		
606	44	1.9				
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608	44	1.9	8952	4	AAS46445	Aas46445 Tumour su
C 609	44	1.9	11964	6	ABQ67026	Abq67026 Human ang
	44	1.9	13627	6	ABQ66975	Abq66975 Human ang
C 611	44	1.9	17674	4	AAS46794	Aas46794 Tumour su
	44	1.9	56153	4	ABQ99654	Abq99654 Human mem
C 612	44	1.9	95109	6	ABL33598	Ab133598 Human imm
C 613	44	1.9	5487	6	ABL34448	Abl34448 Human met
614	43.8	1.8	6127	6	ABL70119	Abl70119 Chemicall
C 615	43.8	1.8	6127	6	AAS46497	Aas46497 Tumour su
C 616	43.8	1.8	6233	4	ABL32323	Ab132323 Human imm
617	43.8	1.8	6418	6	AAS61074	Aas61074 Human gen
C 618	43.8	1.8	6418	6	ABL34541	Abl34541 Human met
C 619	43.8	1.8	6811	6	ABL70264	Ab170264 Chemicall
C 620	43.8	1.8	8093	7	ABZ10178	Abz10178 Haematopo
C 621	43.8	1.8	8093	9	ADB54268	Adb54268 Pretreate
622	43.8	1.8	8093	9	ADE84190	Ade84190 Human lym
623	43.8	1.8	8227	6	ABQ67126	Abq67126 Human ang
624	43.8	1.8	8227	6	ABL34492	Abl34492 Human met
C 625	43.8	1.8	11996	6	ABL34358	Ab134358 Human imm
C 626	43.8	1.8	12237	6	ABL33194	Abl33194 Human imm
627	43.8	1.8	14861	6	ABL70553	Abl70553 Chemicall
C 628	43.8	1.8	14861	6	AAS61202	Aas61202 Human gen
C 629	43.8	1.8	14861	6	AAS46506	Aas46506 Tumour su
C 630	43.8	1.8	14919	4	ABK28395	Abk28395 DNA trans
631	43.8	1.8	15743	6	ABL33090	Ab133090 Human imm
C 632	43.8	1.8	16724	6	ABL34536	Ab134536 Human met
C 633	43.8	1.8	16724	6	ABL70259	Ab170259 Chemicall
C 634	43.8	1.8	16724	6	ABK39952	Abk39952 Human che
C 635	43.8	1.8	17703	6	ABL32254	Abl32254 Human imm
C 636	43.8	1.8	18154	6	ABL32254	Abl32254 Human imm
637	43.8	1.8	18154	6	AAC66747	Aac66747 DNA marke
C 638	43.8	1.8	555	3	ABQ40113	Abq40113 Oligonucl
639	43.6	1.8	583	6	ABQ40112	Abq40112 Oligonucl
C 640	43.6	1.8	583	6	AAK03309	Aak03309 Human bra
C 641	43.6	1.8	1988	4	ABZ10164	Abz10164 Haematopo
642	43.6	1.8	3128	7	ABL34176	Ab134176 Human imm
C 643	43.6	1.8	5368	6	ABL34091	Ab134091 Human imm
C 644	43.6	1.8	5407	6	ABL33870	Ab133870 Human imm
C 645	43.6	1.8	5511	6	ADE84206	Ade84206 Human lym
C 646	43.6	1.8	6028	9	AAS46430	Aas46430 Tumour su
C 647	43.6	1.8	6106	4	ABK40032	Abk40032 Human che
C 648	43.6	1.8	6106	4	ABL33473	Ab133473 Human imm
C 649	43.6	1.8	6106	6	ABL70354	Abl70354 Chemicall
C 650	43.6	1.8	6107	6	AAS61315	Aas61315 Human gen
651	43.6	1.8	6107	6	AAS46574	Aas46574 Tumour su
652	43.6	1.8	6126	4	ABL33831	Ab133831 Human imm
653	43.6	1.8	6126	6	ABL32623	Ab132623 Human imm
654	43.6	1.8	6161	6	ABL33586	Ab133586 Human imm
655	43.6	1.8	6227	6	Ab1922260	Ab1922260 Chemicall
C 656	43.6	1.8	6227	6	Abz79546	Abz79546 Radish Rf
C 657	43.6	1.8	6459	7	AAK86101	Aak86101 Human imm
C 658	43.6	1.8	6558	4	AA137138	Aal37138 Human mus
C 659	43.6	1.8	6558	4	ABA21372	Aba21372 Human ner
C 660	43.6	1.8	6558	7	ABX60126	Abx60126 cDNA enco
C 661	43.6	1.8	6558	5	Abk31451	Abk31451 Signal tr
C 662	43.6	1.8	7131	6	ABL70428	Abl70428 Chemicall
C 663	43.6	1.8	7131	6	AAS61361	Aas61361 Human gen
C 664	43.6	1.8	7131	6	ABL32982	Ab132982 Human imm
C 665	43.6	1.8	7143	6	ABL33775	Ab133775 Human imm
C 666	43.6	1.8	7503	6	ADB54312	Adb54312 Pretreate
C 667	43.6	1.8	7833	9	ADE37779	Ade37779 Human che
C 668	43.6	1.8	7833	9	AAS45432	Aas45432 Chemicall
C 669	43.6	1.8	8866	4	ABK28279	Abk28279 DNA trans
C 670	43.6	1.8	8866	6	ABK28453	Abk28453 DNA trans
C 671	43.6	1.8	10467	6	ADB54222	Adb54222 Pretreate
C 672	43.6	1.8	11913	9	ABL32299	Ab132299 Human imm
C 673	43.6	1.8	12507	6	ABL33712	Ab133712 Human imm
674	43.6	1.8	13326	6	ABL34070	Ab134070 Human imm
675	43.6	1.8	13503	6	AAS46356	Aas46356 Tumour su
C 676	43.6	1.8	14537	4	ABL34469	Ab134469 Human met
677	43.6	1.8	16173	6	ABL33702	Ab133702 Human imm
678	43.6	1.8	18624	6	ABL33933	Ab133933
C 679	43.6	1.8	19734	6		
680	43.6	1.8				

C 681	43.6	1.8	47108	6	ABK31510	Abk31510	Signal tr
C 682	43.6	1.8	50000	6	ABL55644	AmEPV gen	
C 683	43.6	1.8	83391	6	ABQ67093	Human ang	
C 684	43.4	1.8	337	7	ABX41811	Bovine ES	
C 685	43.4	1.8	547	6	ABQ14987	Abq14987	Oligonucle
C 686	43.4	1.8	547	6	ABQ14986	Abq14986	Oligonucle
C 687	43.4	1.8	830	6	ABQ89354	Human pro	
C 688	43.4	1.8	830	8	ADB82297	Human CDN	
C 689	43.4	1.8	2196	6	ABI99480	Mouse isc	
C 690	43.4	1.8	5376	6	ABL34150	Human imm	
C 691	43.4	1.8	6012	6	ABK31491	Signal tr	
C 692	43.4	1.8	6012	6	ABL70464	Chemical	
C 693	43.4	1.8	6106	4	AAS46430	Tumour su	
C 694	43.4	1.8	6106	6	ABK40032	Human che	
C 695	43.4	1.8	6106	6	ABL33473	Human imm	
C 696	43.4	1.8	6317	6	ABL32408	Human imm	
C 697	43.4	1.8	6317	6	ABL49311	Human pol	
C 698	43.4	1.8	6585	6	ABL32832	Human imm	
C 699	43.4	1.8	6585	6	AAS61182	Human gen	
C 700	43.4	1.8	6590	6	ABL33476	Human imm	
C 701	43.4	1.8	6942	6	ABL33735	Human imm	
C 702	43.4	1.8	7903	4	AAS45403	Chemical	
C 703	43.4	1.8	7903	6	ABL33363	Human imm	
C 704	43.4	1.8	7903	6	ABK28248	DNA trans	
C 705	43.4	1.8	8222	7	ACF62816	Colon can	
C 706	43.4	1.8	8222	7	ACF62794	Colon can	
C 707	43.4	1.8	9021	6	ABK40075	Human che	
C 708	43.4	1.8	9021	6	ABL34232	Human imm	
C 709	43.4	1.8	9021	6	ABK33988	Human DNA	
C 710	43.4	1.8	9021	7	ADA20388	Prostate	
C 711	43.4	1.8	9021	7	ADA84195	Human ren	
C 712	43.4	1.8	11222	9	ADB54190	Pretreate	
C 713	43.4	1.8	11222	9	ADB54318	Pretreate	
C 714	43.4	1.8	11422	6	ABK39937	Human che	
C 715	43.4	1.8	11422	6	ABL32219	Human imm	
C 716	43.4	1.8	13427	6	ABL33927	Human imm	
C 717	43.4	1.8	17137	6	ABL32190	Human imm	
C 718	43.4	1.8	24939	6	ABL70570	Chemical	
C 719	43.4	1.8	40324	6	ABQ67150	Human ang	
C 720	43.4	1.8	90541	6	ABS52847	Human SR	
C 721	43.4	1.8	113033	7	AAL54213	SR protei	
C 722	43.2	1.8	469	5	ABV56638	Human pro	
C 723	43.2	1.8	1982	2	AAV40736	C. felis	
C 724	43.2	1.8	1982	2	AAV40735	C. felis	
C 725	43.2	1.8	1982	4	AAD21167	Ctenoceph	
C 726	43.2	1.8	2144	2	AAV40758	C. felis	
C 727	43.2	1.8	2144	2	AAV40759	C. felis	
C 728	43.2	1.8	2144	4	AAD21182	Ctenoceph	
C 729	43.2	1.8	2501	9	ADB54116	Pretreate	
C 730	43.2	1.8	2652	7	ABZ81728	Rat brain	
C 731	43.2	1.8	2652	7	ABZ81727	Rat mutan	
C 732	43.2	1.8	3077	9	ADB59097	Toxicity-	
C 733	43.2	1.8	5294	6	ABL33070	Human imm	
C 734	43.2	1.8	5294	6	ABK31282	Signal tr	
C 735	43.2	1.8	6042	3	AAA70199	Plasmodiu	
C 736	43.2	1.8	6095	4	AAS46310	Tumour su	
C 737	43.2	1.8	6095	6	ABL32361	Human imm	
C 738	43.2	1.8	6095	6	ABL34475	Human met	
C 739	43.2	1.8	6095	6	ABL70150	Chemical	
C 740	43.2	1.8	6285	6	ABL33496	Human imm	
C 741	43.2	1.8	6286	4	AAS46591	Tumour su	
C 742	43.2	1.8	6641	6	ABL32315	Human imm	
C 743	43.2	1.8	6641	6	ABL54336	Chemical	
C 744	43.2	1.8	6880	6	ABK31323	Signal tr	
C 745	43.2	1.8	6880	6	ABL70294	Chemical	
C 746	43.2	1.8	6880	6	AAS61224	Human gen	
C 747	43.2	1.8	10710	6	ABL32893	Human imm	
C 748	43.2	1.8	11670	6	ABL54326	Chemical	
C 749	43.2	1.8	13712	6	ABL33531	Human imm	
C 750	43.2	1.8	14307	6	ABL32729	Human imm	
C 751	43.2	1.8	15373	6	ABL32467	Human imm	
C 752	43.2	1.8	16217	6	ABL32625	Human imm	
C 753	43.2	1.8	17594	6	ABL34027	Human imm	

C 754	43.2	1.8	20674	3	AAC58017	Aac58017	Arachidon
755	43.2	1.8	24939	6	ABL70570	Chemical	
756	43.2	1.8	74586	6	AAS16905	Genomic D	
757	43	1.8	1132	6	ABZ15647	Arabidops	
C 758	43	1.8	5218	6	ABL33266	Human imm	
759	43	1.8	5942	6	ABK33945	Human DNA	
760	43	1.8	5942	6	ABK31223	Signal tr	
761	43	1.8	5942	6	ABL70534	Chemical	
762	43	1.8	5942	6	AAS61135	Human gen	
763	43	1.8	5942	7	ABZ10002	Haematopo	
764	43	1.8	5942	7	ABZ10234	Haematopo	
765	43	1.8	5942	7	ABZ10088	Haematopo	
766	43	1.8	5942	7	ABZ10148	Haematopo	
767	43	1.8	5942	7	ADA20351	Prostate	
768	43	1.8	5942	7	ADA84158	Human ren	
769	43	1.8	5942	9	ADE84068	Human lym	
770	43	1.8	5942	9	ADE84144	Human lym	
C 771	43	1.8	6077	6	ABL33246	Human imm	
C 772	43	1.8	6126	4	AAS46573	Tumour su	
C 773	43	1.8	6126	6	ABL33830	Human imm	
C 774	43	1.8	6233	4	AAS46498	Tumour su	
C 775	43	1.8	6317	6	ABL32409	Human imm	
C 776	43	1.8	6317	6	ABL49312	Human pol	
777	43	1.8	7441	6	ABK40057	Human che	
778	43	1.8	7479	6	AAS63344	Chemical	
C 779	43	1.8	7900	4	AAS46760	Tumour su	
C 780	43	1.8	8592	6	ABL33983	Human imm	
C 781	43	1.8	9810	6	ABL32427	Human imm	
C 782	43	1.8	11787	6	ABL92243	Chemical	
C 783	43	1.8	11787	9	ADB54202	Pretreate	
C 784	43	1.8	13574	6	ABL33316	Human imm	
C 785	43	1.8	16228	6	ABL70459	Chemical	
C 786	43	1.8	16228	6	AAS61424	Human gen	
C 787	43	1.8	16579	9	ADB54118	Pretreate	
C 788	43	1.8	16579	9	ADE37763	Human che	
C 789	43	1.8	19082	6	ABL32627	Human imm	
C 790	43	1.8	19082	6	ABL32627	Human imm	
C 791	43	1.8	20933	6	ABQ67124	Human ang	
C 792	43	1.8	29993	9	ADB37661	Human che	
C 793	43	1.8	37184	6	ABQ67078	Human ang	
C 794	43	1.8	38342	4	AAS46746	Tumour su	
C 795	43	1.8	38342	6	ABK31507	Signal tr	
C 796	43	1.8	50000	6	ABL56202	AmEPV gen	
C 797	42.8	1.8	2000	6	ABZ16071	Arabidops	
C 798	42.8	1.8	5204	6	ABL32899	Human imm	
C 799	42.8	1.8	5454	3	AAA70236	Plasmodiu	
C 800	42.8	1.8	5611	6	ABQ67069	Human ang	

ALIGNMENTS

RESULT 1

AAAX52250
ID AAAX52250 standard; DNA; 2372 BP.

XX AC AAAX52250;

XX AC AAAX52250;

DT 25-JUN-1999 (first entry)

XX Protein PRO263 cDNA clone DNA34431-1171.

XX Secreted protein; transmembrane protein; human; enterocolitis;

KW Zollinger-Ellison syndrome; gastrointestinal ulceration;

KW congenital microvillus atrophy; skin disease; cell growth;

KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;

KW parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;

KW dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;

XX wound healing; tissue repair; ss.

OS Homo sapiens.

XX OS Homo sapiens.

PN WO9914328-A2.

[illegible]

QY 781 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTTGTGAAATAAAGCAGCATTC AAG 840
Db 781 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTTGTGAAATAAAGCAGCATTC AAG 840
QY 841 AATGAAGCTGCTGGGTTTGAGGTTGTCCTCCACCGGCTCTGCTAGTGCTTCTCTTC 900
Db 841 AATGAAGCTGCTGGGTTTGAGGTTGTCCTCCACCGGCTCTGCTAGTGCTTCTCTTC 900
QY 901 TTTGGTGTGCAGCTGGTCTTGGAATTTTGCTATGTCAAAGGTATGTGAAGGCTTCCCT 960
Db 901 TTTGGTGTGCAGCTGGTCTTGGAATTTTGCTATGTCAAAGGTATGTGAAGGCTTCCCT 960
QY 961 TTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACCAAAAGTAGTAAAGGAGGAAG 1020
Db 961 TTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACCAAAAGTAGTAAAGGAGGAAG 1020
QY 1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACCTGATAAAAACCCAGAGTCC 1080
Db 1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACCTGATAAAAACCCAGAGTCC 1080
QY 1081 AAGAGTCCAAGCABAACTACCGTCGATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140
Db 1081 AAGAGTCCAAGCABAACTACCGTCGATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140
QY 1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCTTACCTGCCCCAGCTGGGAA 1200
Db 1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCTTACCTGCCCCAGCTGGGAA 1200
QY 1201 ATCAAAAGGGCCAAAGAACCAAGAAAGTCCACCTTGTTCTTAACTGGAATCAGC 1260
Db 1201 ATCAAAAGGGCCAAAGAACCAAGAAAGTCCACCTTGTTCTTAACTGGAATCAGC 1260
QY 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGATGCCCTTCTCCTTATTGTAAC 1320
Db 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGATGCCCTTCTCCTTATTGTAAC 1320
QY 1321 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT 1380
Db 1321 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT 1380
QY 1381 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTGTGCAAAAGTCAAGGACCTAAAACATC 1440
Db 1381 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTGTGCAAAAGTCAAGGACCTAAAACATC 1440
QY 1441 TCATCAGTATCCAGTGGTAAAGGGCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1500
Db 1441 TCATCAGTATCCAGTGGTAAAGGGCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1500
QY 1501 CAAGGAGTCACTGAGACCAAGGTTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
Db 1501 CAAGGAGTCACTGAGACCAAGGTTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
QY 1561 GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTGAGCCCGGTAAGAGCAAA 1620
Db 1561 GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTGAGCCCGGTAAGAGCAAA 1620
QY 1621 AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680
Db 1621 AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680
QY 1681 TCTCTGTAAAGCTAAAATAAAGAAATAGAAACAAGGCTAGGATACGACAGTACACTGTCA 1740
Db 1681 TCTCTGTAAAGCTAAAATAAAGAAATAGAAACAAGGCTAGGATACGACAGTACACTGTCA 1740
QY 1741 GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTTCTGAACACATTGAGTTGGAAT 1800
Db 1741 GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTTCTGAACACATTGAGTTGGAAT 1800
QY 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTTACCACTGCTGATATTTCTCT 1860
Db 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTTACCACTGCTGATATTTCTCT 1860

QY 1861 AGGAAATATACTTTTACAAGTAACAAAAATAAAAACCTTATATAAATTTCTATTTTATCT 1920
Db 1861 AGGAAATATACTTTTACAAGTAACAAAAATAAAAACCTTATATAAATTTCTATTTTATCT 1920
QY 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAA 1980
Db 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAA 1980
QY 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTC 2040
Db 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTC 2040
QY 2041 TGTAAATTGAATATTATTCCTCAAAAATTTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
Db 2041 TGTAAATTGAATATTATTCCTCAAAAATTTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
QY 2101 TTTTTCAGTTTGTGATTTTCTAGCTTATCTACTTCCAAAATAATTTTATTTTGTCTGA 2160
Db 2101 TTTTTCAGTTTGTGATTTTCTAGCTTATCTACTTCCAAAATAATTTTATTTTGTCTGA 2160
QY 2161 GACTAATCTTATTCATTTTCTTAATATGGCAACCATTAATATAACCTTAATTTATTATAAC 2220
Db 2161 GACTAATCTTATTCATTTTCTTAATATGGCAACCATTAATATAACCTTAATTTATTATAAC 2220
QY 2221 ATACCTAAGAAGTACATTGTTACCTCTATATACCAAAGCACATTTTAAAAAGTGCCATTAA 2280
Db 2221 ATACCTAAGAAGTACATTGTTACCTCTATATACCAAAGCACATTTTAAAAAGTGCCATTAA 2280
QY 2281 CAAATGTATCACTAGCCCTCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAATATT 2340
Db 2281 CAAATGTATCACTAGCCCTCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAATATT 2340
QY 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372
Db 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372

RESULT 2

ADC78520

ID ADC78520 standard; cDNA; 2372 BP.

XX

AC ADC78520;

XX 01-JAN-2004 (first entry)

XX Human PRO263 cDNA.

DE

XX antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;

KW nootropic; neuroprotective; vasotropic; chemotaxic; angiogenic;

KW neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;

KW antiarteriosclerotic; cardiant; antidiabetic; cerebroprotective;

KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;

KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;

KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;

KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;

KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;

KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;

KW diabetes; stroke; gene therapy; transgenic; PRO; human; ss; gene.

XX Homo sapiens.

OS WO200015796-A2.

XX 23-MAR-2000.

XX 15-SEP-1999; 99WO-US021090.

XX 16-SEP-1998; 98WO-US019330.

XX (GETH) GENENTECH INC.

XX Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;

PI Yuan J;

WPI; 2000-271434/23.
P-PSDB; ADC78521.

Novel nucleic acids encoding secreted and transmembrane polypeptides with homology, e.g. to growth and cancer-associated antigens.

Claim 2; SEQ ID NO 200; 355pp; English.

The invention relates to a novel nucleic acid encoding a PRO polypeptide. The polypeptides and polynucleotides of the invention may be useful as research tools and as therapeutics for treating enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer, Parkinson's disease, Alzheimer's disease, ALS, neuropathies, cancer, scarring and wound healing, nerve repair, thrombosis, bone and/or cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple sclerosis, inflammatory disorders, atherosclerosis, cardiac injury, infertility, premature aging, AIDS, diabetes complications and stroke. The molecules may also be utilised during gene therapy procedures and transgenic animal production. The current sequence is that of the human PRO cDNA of the invention.

Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 3; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AGCAGGGAAATCCGGATGTCCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA	60
Db	1	AGCAGGGAAATCCGGATGTCCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA	60
QY	61	GTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC	120
Db	61	GTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC	120
QY	121	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCAGGTGCTTCAGCCTG	180
Db	121	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCAGGTGCTTCAGCCTG	180
QY	181	GTGTTGCTTCTCACTTCCATCTGGACCCAGAGGCTCCTGGTCCAAGGCTCTTTGGGTGCA	240
Db	181	GTGTTGCTTCTCACTTCCATCTGGACCCAGAGGCTCCTGGTCCAAGGCTCTTTGGGTGCA	240
QY	241	GAAGAGCTTTCATCCAGGTGTCATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAG	300
Db	241	GAAGAGCTTTCATCCAGGTGTCATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAG	300
QY	301	GCGAACCCAGCAGCTGAATTCACAGAAGCTAAGGAGGCTGTAGGCTGCTGGACTAAGT	360
Db	301	GCGAACCCAGCAGCTGAATTCACAGAAGCTAAGGAGGCTGTAGGCTGCTGGACTAAGT	360
QY	361	TTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	420
Db	361	TTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	420
QY	421	GGCTGGTTGGAGATGGATTTCGTGGTCACTCTAGGATTAGCCAAACCCCAAGTGTGG	480
Db	421	GGCTGGTTGGAGATGGATTTCGTGGTCACTCTAGGATTAGCCAAACCCCAAGTGTGG	480
QY	481	AAAAATGGGTGGGTGTCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	540
Db	481	AAAAATGGGTGGGTGTCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	540
QY	541	TGTTACAACACTCATCTGATACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAA	600
Db	541	TGTTACAACACTCATCTGATACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAA	600
QY	601	GATCCCATATTCAACACTCAAACTGCAACACAAACACAGATTATTGTGAGTGACAGT	660
Db	601	GATCCCATATTCAACACTCAAACTGCAACACAAACACAGATTATTGTGAGTGACAGT	660
QY	661	ACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCCCTACTACTCTCCTCTGCT	720

Db	1741	GCAGG	ACTGTA	AAACAC	AGACAG	AGGGTCAA	AGTGTCTCT	CTGA	CACAT	TGAGTT	GGAAT	1800	
Qy	1801	CAC	TGTT	TAGAA	CACAC	CACACT	TACTTTTT	CTGGT	CTCTAC	CACTG	CTGAF	TTTTCTCT	1860
Db	1801	CAC	TGTT	TAGAA	CACAC	CACACT	TACTTTTT	CTGGT	CTCTAC	CACTG	CTGAF	TTTTCTCT	1860
Qy	1861	AGG	AAAT	ATA	CTTTT	TACA	AGTAACA	AAAAAT	AAAAAA	CTCT	TATA	AAATTTCT	1920
Db	1861	AGG	AAAT	ATA	CTTTT	TACA	AGTAACA	AAAAAT	AAAAAA	CTCT	TATA	AAATTTCT	1920
Qy	1921	GAG	TTAC	AGAA	ATGATT	ACT	TAAGGA	AGATT	TACT	CAGT	AAATTTG	TTAAAAAG	1980
Db	1921	GAG	TTAC	AGAA	ATGATT	ACT	TAAGGA	AGATT	TACT	CAGT	AAATTTG	TTAAAAAG	1980
Qy	1981	TTCA	ACAA	CAATTT	GTCT	GAATAG	CTACT	ATAT	TCTCA	AGTGTCT	GTGCA	AGGTATT	2040
Db	1981	TTCA	ACAA	CAATTT	GTCT	GAATAG	CTACT	ATAT	TCTCA	AGTGTCT	GTGCA	AGGTATT	2040
Qy	2041	TGTA	ATTG	AA	TATAT	TCTC	CAAAAA	ATTG	CACAT	AGTAG	AACGCT	ATCTGG	2100
Db	2041	TGTA	ATTG	AA	TATAT	TCTC	CAAAAA	ATTG	CACAT	AGTAG	AACGCT	ATCTGG	2100
Qy	2101	TTTT	TTT	CAG	TTTT	GAT	ATTTCT	AGCT	TATCT	ACTTCC	AAACT	TAATTTT	2160
Db	2101	TTTT	TTT	CAG	TTTT	GAT	ATTTCT	AGCT	TATCT	ACTTCC	AAACT	TAATTTT	2160
Qy	2161	GAC	TAA	CTTA	TTCA	TTTCT	CTAAT	TGGCA	ACCATT	TATA	ACCTTA	ATTTATT	2220
Db	2161	GAC	TAA	CTTA	TTCA	TTTCT	CTAAT	TGGCA	ACCATT	TATA	ACCTTA	ATTTATT	2220
Qy	2221	ATAC	CTA	AG	AGTAC	ATTG	TTAC	CTCT	ATAT	ATCC	AAAGCAC	ATTTT	2280
Db	2221	ATAC	CTA	AG	AGTAC	ATTG	TTAC	CTCT	ATAT	ATCC	AAAGCAC	ATTTT	2280
Qy	2281	CAA	ATG	TATC	ACTAG	CCCTC	CTTTT	TTCC	AAACA	AGGG	ACTGAG	AGATGC	2340
Db	2281	CAA	ATG	TATC	ACTAG	CCCTC	CTTTT	TTCC	AAACA	AGGG	ACTGAG	AGATGC	2340
Qy	2341	TGT	GAC	AAAA	AAATTA	AAG	CAATTT	TAG	AAAA	CTT			2372
Db	2341	TGT	GAC	AAAA	AAATTA	AAG	CAATTT	TAG	AAAA	CTT			2372

RESULT 3
AAE72408

ID AAF72408 standard; cDNA; 2372 BP.

AC AAF72408;

DT 24-APR-2001 (first entry)

Human PRO263 cDNA.

KW Human; PRO; dermat

antiparkinsonian, neurotrophic; neuroprotection; neuroregeneration; cancer;
KW antiangiogenic; vasoprotective; antiasthmatic; antirheumatic; cancer;
KW antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation; ss.

OS Homo sapiens.

PN WO200104311-A1.

PD 18~JAN-2001.

PF 22-FEB-2000; 2000WO-US004414.

PR 07-JUL-1999; 99US-0143048P.

PR 28-JUL-1999; 99US-0146222P.

PR 13-SEP-1999; 99WO-US020944.

PR	15-SEP-1999;	99WO-US021090.
PR	15-SEP-1999;	99WO-US021547.
PR	05-OCT-1999;	99WO-US023089.
PR	29-NOV-1999;	99WO-US028214.
PR	30-NOV-1999;	99WO-US028313.
PR	02-DEC-1999;	99WO-US028564.
PR	02-DEC-1999;	99WO-US028565.
PR	16-DEC-1999;	99WO-US030095.
PR	20-DEC-1999;	99WO-US030911.
PR	20-DEC-1999;	99WO-US030999.
PR	05-JAN-2000;	2000WO-US000219.

PA (GETH) GENENTECH INC.

PI	Ashkenazi AJ,	Botstein D,	Desnovers L,	Eaton DL,	Ferrara N;
PI	Filvaroff E,	Fong S,	Gao W,	Gerber H,	Gerritsen ME,
PI	Godowski PJ,	Grimaldi CJ,	Gurney AL,	Hillan KJ,	Kljavin IJ;
PI	Mather JP,	Pan J,	Paoni NF,	Roy MA,	Stewart TA,
PI	Williams PM,	Wood WI;			Tumas D;

DR WPI; 2001-081051/09.
DR P-PSDB; AAB80247.

Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's disease).

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 4; Length 2372;

Matches 2372; Conservative 0; Mismatches

QV 1 AGCAGGAAATCCGGATGTCCTGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60

Db
1 AGCAGGGAATCCGGATGTCGGTTATGAAGTGAGCAGTGAGTGTGAGCCTCAACATA 60

QY 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCTCATATCACCAGTGGC 120

Db 61 GTTCCAGAACTCTCCATCCGGA CTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120

QY 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180

Db 121 CATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180

QY 181 GTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGTCCAAGGCTCTTTGCGTGCA 240

Db 181 GTGTTGCTTCTCACTTCCATCTGGACCAAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240

Qy 241 GAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAG 300

Db 241 GAAGAGCTTCCATCCAGGTGTCATGCAGAAATTATGGGATCACCCCTTGTCAGCAAAAAG 300

QY 301 GCGAAC CAGCAGCTGAATTT CACAGAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGT 360

Db 301 GCGAAC CAGCAGCTGAATTTACAGAGCTAAGGAGCCCTGTAGGCTGCTGGACTAAGT 360

QY 361 TTGGCCGCAAGGACCAAGTTGAAACACAGCCCTGAAAGCTAGCTTTGAAAACCTTGCAGCTAT 420
Db |||||
361 TTGGCCGCAAGGACCAAGTTGAAACACAGCCCTGAAAGCTAGCTTTGAAAACCTTGCAGCTAT 420
QY 421 GGCTGGGTTGGAGATGGATTTCGTGGTGCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGG 480
Db |||||
421 GGCTGGGTTGGAGATGGATTTCGTGGTGCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGG 480
QY 481 AAAAAATGGGTGGGTGTCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
Db |||||
481 AAAAAATGGGTGGGTGTCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
QY 541 TGTACAACTCATCTGATACCTTGGACTAACTCGTGCAATCCAGAAATATCACCACCAA 600
Db |||||
541 TGTACAACTCATCTGATACCTTGGACTAACTCGTGCAATCCAGAAATATCACCACCAA 600
QY 601 GATCCCATATTCAACACTCAAACCTGCAACACAAAACAGAAATTTATTTGTCAGTGACAGT 660
Db |||||
601 GATCCCATATTCAACACTCAAACCTGCAACACAAAACAGAAATTTATTTGTCAGTGACAGT 660
QY 661 ACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCTACTACTACTCCTCCTGCT 720
Db |||||
661 ACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCTACTACTACTCCTCCTGCT 720
QY 721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTTGTCACAGAAAGTTTTTATG 780
Db |||||
721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTTGTCACAGAAAGTTTTTATG 780
QY 781 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTTCAAG 840
Db |||||
781 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTTCAAG 840
QY 841 AATGAAGCTGCTGGGTTTGGAGTGTCCCCACGGCTCTGCTAGTGTGCTCTCCTCTTC 900
Db |||||
841 AATGAAGCTGCTGGGTTTGGAGTGTCCCCACGGCTCTGCTAGTGTGCTCTCCTCTTC 900
QY 901 TTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAAAGGATGTGAAGGCCCTCCCT 960
Db |||||
901 TTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAAAGGATGTGAAGGCCCTCCCT 960
QY 961 TTTACAAAACAAGAAATCAGCAGAAAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAG 1020
Db |||||
961 TTTACAAAACAAGAAATCAGCAGAAAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAG 1020
QY 1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACCTGATAAAAACCCAGAAGTCC 1080
Db |||||
1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACCTGATAAAAACCCAGAAGTCC 1080
QY 1081 AAGAGTCCAAGCAAAAACCTACCGTGGATGCTGGAAGCTGAAGTTAGATGAGACAGAAA 1140
Db |||||
1081 AAGAGTCCAAGCAAAAACCTACCGTGGATGCTGGAAGCTGAAGTTAGATGAGACAGAAA 1140
QY 1141 TGAGGAGACACACCTGAGGCTGGTTCTTTTCATGCTCCTTACCCCTGCCCTGCCAGCTGGGAA 1200
Db |||||
1141 TGAGGAGACACACCTGAGGCTGGTTCTTTTCATGCTCCTTACCCCTGCCCTGCCAGCTGGGAA 1200
QY 1201 ATCAAAAAGGCCAAAGAACCAAGAGAAAGTCCACCCCTTGGTTCCTAACTGGAATCAGC 1260
Db |||||
1201 ATCAAAAAGGCCAAAGAACCAAGAGAAAGTCCACCCCTTGGTTCCTAACTGGAATCAGC 1260
QY 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1320
Db |||||
1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1320
QY 1321 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCTTTCTAGCCTGGCTAT 1380
Db |||||
1321 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCTTTCTAGCCTGGCTAT 1380
QY 1381 GTCCTAATAATATCCCACCTGGGAGAAAGGAGTTTTCGCAAGTGCAGGACCTAAAAACATC 1440
Db |||||
1381 GTCCTAATAATATCCCACCTGGGAGAAAGGAGTTTTCGCAAGTGCAGGACCTAAAAACATC 1440
QY 1441 TCATCAGTATCCAGTGGTAAAAAAGGCCCTCCTGGCTGTCTGAGCTAGGTGGGTTGAAAGC 1500

Db 1441 TCATCAGTATCCAGTGGTAAAAAGGCTCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGC 1500
QY 1501 CAAGGAGTCACTGAGACCAGGCTTTCTCTACTGATTCCGCAGCTCAGACCCCTTTCTTCA 1560
Db |||||
1501 CAAGGAGTCACTGAGACCAGGCTTTCTCTACTGATTCCGCAGCTCAGACCCCTTTCTTCA 1560
QY 1561 GCTCTGAAAAGAGAAAACACGTCATCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAA 1620
Db |||||
1561 GCTCTGAAAAGAGAAAACACGTCATCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAA 1620
QY 1621 AGAATGCGAGAAAAAGTTTAGCCCTGAAAAGCCCATGGAGATTCTCATAACTTGAGACCTAA 1680
Db |||||
1621 AGAATGCGAGAAAAAGTTTAGCCCTGAAAAGCCCATGGAGATTCTCATAACTTGAGACCTAA 1680
QY 1681 TCTCTGTAAAGCTAAAAATAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACTGTCA 1740
Db |||||
1681 TCTCTGTAAAGCTAAAAATAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACTGTCA 1740
QY 1741 GCAGGACTGTAAACACACAGACAGGCTCAAAGTGTCTTCTGAAACACATTTGGAAT 1800
Db |||||
1741 GCAGGACTGTAAACACACAGACAGGCTCAAAGTGTCTTCTGAAACACATTTGGAAT 1800
QY 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860
Db |||||
1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860
QY 1861 AGGAAATATACTTTTACAAGTAAACAAAAATAAAAACCTCTTATAAATTTCTATTTTATCT 1920
Db |||||
1861 AGGAAATATACTTTTACAAGTAAACAAAAATAAAAACCTCTTATAAATTTCTATTTTATCT 1920
QY 1921 GAGTTACAGAAAATGATTACTTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAA 1980
Db |||||
1921 GAGTTACAGAAAATGATTACTTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAA 1980
QY 1981 TTCAACAAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTC 2040
Db |||||
1981 TTCAACAAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTC 2040
QY 2041 TGTAAATTGAATATTATTCCTCAAAAAAATGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
Db |||||
2041 TGTAAATTGAATATTATTCCTCAAAAAAATGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
QY 2101 TTTTTCAGTTCCTGATATTTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTCTGA 2160
Db |||||
2101 TTTTTCAGTTCCTGATATTTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTCTGA 2160
QY 2161 GACTAATCTTATTCATTTTCTTAATATGGCAACCATTTATAACCTTAATTTATTTAAC 2220
Db |||||
2161 GACTAATCTTATTCATTTTCTTAATATGGCAACCATTTATAACCTTAATTTATTTAAC 2220
QY 2221 ATACCTAAGAAGTACATTTGTACCTCTATATACCAAGCACATTTTAAAGTGCCATTA 2280
Db |||||
2221 ATACCTAAGAAGTACATTTGTACCTCTATATACCAAGCACATTTTAAAGTGCCATTA 2280
QY 2281 CAAATGTATCACTAGCCCTCCTTTTCCAACAAGAGGACTGAGAGATGCAGAAAAATTT 2340
Db |||||
2281 CAAATGTATCACTAGCCCTCCTTTTCCAACAAGAGGACTGAGAGATGCAGAAAAATTT 2340
QY 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372
Db |||||
2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372

RESULT 4
AAF92060
ID AAF92060 standard; cDNA; 2372 bp.
XX
AC AAF92060;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO263 cDNA.

Db 1321 CCTGTCGGATCCTATCCTCTACCTCCAAAGCTTCCCACGCGCTTTCTAGCCTGGCTAT 1380
QY 1381 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTTGCAAGTGC AAGGACCTAAAAACATC 1440
Db 1381 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTTGCAAGTGC AAGGACCTAAAAACATC 1440
QY 1441 TCATCAGTATCCAGTGGTAAAGGCTCCTGGCTGTCGAGGCTAGGTGGGTTGAAAGC 1500
Db 1441 TCATCAGTATCCAGTGGTAAAGGCTCCTGGCTGTCGAGGCTAGGTGGGTTGAAAGC 1500
QY 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATCCGAGCTCAGACCCCTTTCTTCA 1560
Db 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATCCGAGCTCAGACCCCTTTCTTCA 1560
QY 1561 GCTCTGAAAGAGAAACACGATATCCACCTGACATGTCTTCTGAGCCCGGTAAAGGCAAA 1620
Db 1561 GCTCTGAAAGAGAAACACGATATCCACCTGACATGTCTTCTGAGCCCGGTAAAGGCAAA 1620
QY 1621 AGAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680
Db 1621 AGAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680
QY 1681 TCTCTGTAAAGCTAAATTAAGAAATAGAAC AAGGCTGAGGATACGACAGTACACTGTCA 1740
Db 1681 TCTCTGTAAAGCTAAATTAAGAAATAGAAC AAGGCTGAGGATACGACAGTACACTGTCA 1740
QY 1741 GCAGGGACTGTAAACACAGACAGAGGCTCAAAGTGTCTTCTCTGAACACATTGAGTTGGAAT 1800
Db 1741 GCAGGGACTGTAAACACAGACAGAGGCTCAAAGTGTCTTCTCTGAACACATTGAGTTGGAAT 1800
QY 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860
Db 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860
QY 1861 AGGAAATATACCTTTTACAAGTAACAAAAATAAAAACCTCTTATAAATTTCTATTTTATCT 1920
Db 1861 AGGAAATATACCTTTTACAAGTAACAAAAATAAAAACCTCTTATAAATTTCTATTTTATCT 1920
QY 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAAATTTGTTTAAAAAGTAAFAAAA 1980
Db 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAAATTTGTTTAAAAAGTAAFAAAA 1980
QY 1981 TTCAACAAACATTTGCTGAATAGCTACTATATATGTC AAGTGTGCAAGGTATTACACTC 2040
Db 1981 TTCAACAAACATTTGCTGAATAGCTACTATATATGTC AAGTGTGCAAGGTATTACACTC 2040
QY 2041 TGTAATTGAATATTTCTCTCAAAAAATTTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
Db 2041 TGTAATTGAATATTTCTCTCAAAAAATTTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
QY 2101 TTTTTCAGTTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTTTGTCTGA 2160
Db 2101 TTTTTCAGTTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTTTGTCTGA 2160
QY 2161 GACTAATCTTATTCATTTTCTCTAATATGGCAACCAATTATAACCTTAATTTTATTAATAAC 2220
Db 2161 GACTAATCTTATTCATTTTCTCTAATATGGCAACCAATTATAACCTTAATTTTATTAATAAC 2220
QY 2221 ATACCTAAGAAGTACATTTGTACCTCTATATACCAAGACACATTTTAAAAAGTGCCATTAA 2280
Db 2221 ATACCTAAGAAGTACATTTGTACCTCTATATACCAAGACACATTTTAAAAAGTGCCATTAA 2280
QY 2281 CAAATGTATCACTAGCCCTCCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAATATT 2340
Db 2281 CAAATGTATCACTAGCCCTCCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAATATT 2340
QY 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372
Db 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372

ABS74380
ID ABS74380 standard; cDNA; 2372 BP.
XX
AC ABS74380;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO263.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN US2002119130-A1.
XX
PD 29-AUG-2002.
XX
PF 06-DEC-2001; 2001US-00006867.
XX
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 29-APR-1998; 98US-0083495P.
PR 15-MAY-1998; 98US-0085579P.
PR 02-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 11-JUN-1998; 98US-0088863P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089653P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 24-JUN-1998; 98US-0090444P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 02-JUL-1998; 98US-0091628P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097979P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99WO-US005028.

PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2002-731348/79.
DR P-PSDB; ABG95853.
XX
PT New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating sports-related
PT joint problems, osteoarthritis or rheumatoid arthritis.
XX
PS Claim 2; Fig 5; 399pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide
CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation

CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence encodes a novel secreted or transmembrane protein of the
CC invention
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCAGGGAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCCTCAACATA 60
Db |||||
1 AGCAGGGAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCCTCAACATA 60

QY 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
Db |||||
61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120

QY 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
Db |||||
121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180

QY 181 GTGTTGCTTCTCATTCCATCTGGACCACGAGGCTCTCTGGTCCAAGGCTCTTTGCGTGCA 240
Db |||||
181 GTGTTGCTTCTCATTCCATCTGGACCACGAGGCTCTCTGGTCCAAGGCTCTTTGCGTGCA 240

QY 241 GAAGAGCTTTCATCCAGGTGTCTATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAG 300
Db |||||
241 GAAGAGCTTTCATCCAGGTGTCTATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAG 300

QY 301 GCGAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCTGTAGGCTGTGGGACTAAGT 360
Db |||||
301 GCGAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCTGTAGGCTGTGGGACTAAGT 360

QY 361 TTGGCCGGCAAGGACCAAGTTGAAAACAGCCCTTGAAGAGTAGCTTTGAAAACCTGCAGCTAT 420
Db |||||
361 TTGGCCGGCAAGGACCAAGTTGAAAACAGCCCTTGAAGAGTAGCTTTGAAAACCTGCAGCTAT 420

QY 421 GGCTGGGTTGGAGATGGATTGTTGGTTCATCTCTAGATTAGCCCAACCCCAAGTGGG 480
Db |||||
421 GGCTGGGTTGGAGATGGATTGTTGGTTCATCTCTAGATTAGCCCAACCCCAAGTGGG 480

QY 481 AAAAATGGGGTGGTGCTCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCTAT 540
Db |||||
481 AAAAATGGGGTGGTGCTCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCTAT 540

QY 541 TGTTACAACTCATCTGATCTGGACTAACTCGTGATTCAGAAATTATCACCACAAA 600
Db |||||
541 TGTTACAACTCATCTGATCTGGACTAACTCGTGATTCAGAAATTATCACCACAAA 600

QY 601 GATCCCATATTCACACTCAAACTGCAACACAAACAGAAATTTATTGTGAGTACAGT 660
Db |||||
601 GATCCCATATTCACACTCAAACTGCAACACAAACAGAAATTTATTGTGAGTACAGT 660

QY 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTCTCTCTGCT 720
Db |||||
661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTCTCTCTGCT 720

QY 721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTGTGTACAGAAAGTTTATG 780
Db |||||
721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTGTGTACAGAAAGTTTATG 780

QY 781 GAAACTAGCACCATGTCTACAGAACTGAACCAATTTGTGAAAAATAAGCAGCATTCAG 840
Db |||||
781 GAAACTAGCACCATGTCTACAGAACTGAACCAATTTGTGAAAAATAAGCAGCATTCAG 840

QY 841 AATGAAGCTGTGGGTTTGGAGGTGTCCCAACGGCTGTGCTTAGTGTCTCTCTCTTC 900
Db |||||

Db 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGTCTAGTGTGCTCTCCTCTTC 900

QY 901 TTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCT 960

Db 901 TTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCT 960

QY 961 TTTACAACAAGAATCAGCAGAAAGGAATGATCGAAACCAAAAGTAGTAAAGGAGGAAG 1020

Db 961 TTTACAACAAGAATCAGCAGAAAGGAATGATCGAAACCAAAAGTAGTAAAGGAGGAAG 1020

QY 1021 GCCAATGATAGCAACCCCTAATGAGGGAATCAAAAGAAACTGATAAAAAACCCAGAAGTCC 1080

Db 1021 GCCAATGATAGCAACCCCTAATGAGGGAATCAAAAGAAACTGATAAAAAACCCAGAAGTCC 1080

QY 1081 AAGAGTCCAAGCAAAACTACCGTGGGATGCCCTGGAAGCTGAAAGCTGAAAGTTAGATGAGACAGAA 1140

Db 1081 AAGAGTCCAAGCAAAACTACCGTGGGATGCCCTGGAAGCTGAAAGCTGAAAGTTAGATGAGACAGAA 1140

QY 1141 TGAGGAGACACACTGAGGCTGGTTTCTTTTCATGCTCCTTACCGTCCCCCAGCTGGGAA 1200

Db 1141 TGAGGAGACACACTGAGGCTGGTTTCTTTTCATGCTCCTTACCGTCCCCCAGCTGGGAA 1200

QY 1201 ATCAAAAGGGCCAAAGAACCAAGAAGAAAAGTCCACCCCTTGTTCTTAAGTGAATCAGC 1260

Db 1201 ATCAAAAGGGCCAAAGAACCAAGAAGAAAAGTCCACCCCTTGTTCTTAAGTGAATCAGC 1260

QY 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAATGCCCTTCTCCTTATTGTAAAC 1320

Db 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAATGCCCTTCTCCTTATTGTAAAC 1320

QY 1321 CCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCCTGGCTAT 1380

Db 1321 CCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCCTGGCTAT 1380

QY 1381 GTCCTAATAATATCCCACCTGGGAGAAAGGAGTTTGTGCAAGTGCAAAGGACCTAAACATC 1440

Db 1381 GTCCTAATAATATCCCACCTGGGAGAAAGGAGTTTGTGCAAGTGCAAAGGACCTAAACATC 1440

QY 1441 TCATCAGTATCCAGTGGTAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1500

Db 1441 TCATCAGTATCCAGTGGTAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1500

QY 1501 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560

Db 1501 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560

QY 1561 GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTAAAGCAAA 1620

Db 1561 GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTAAAGCAAA 1620

QY 1621 AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680

Db 1621 AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680

QY 1681 TCTCTGTAAAGCTAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1740

Db 1681 TCTCTGTAAAGCTAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1740

QY 1741 GCAGGGACTGTAAACACACAGACAGGGTCAAAGTGTCTTCTGAAACACATTGAGTTGGAAT 1800

Db 1741 GCAGGGACTGTAAACACACAGACAGGGTCAAAGTGTCTTCTGAAACACATTGAGTTGGAAT 1800

QY 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860

Db 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860

QY 1861 AGGAAATATACCTTTTACAAGTAAACAAAACCTTATATAAAATTTCTATTTTATCT 1920

Db 1861 AGGAAATATACCTTTTACAAGTAAACAAAACCTTATATAAAATTTCTATTTTATCT 1920

QY 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980

Db 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980

QY 1981 TTCAACAACAACATTTGCTGAATAGCTACTATATGTCAAGTGTCTGCAAGGTATTACACTC 2040

Db 1981 TTCAACAACAACATTTGCTGAATAGCTACTATATGTCAAGTGTCTGCAAGGTATTACACTC 2040

QY 2041 TGTAATTGAATATTATTCTCCCAAAAATTCACATAGTAGAACGCTATCTGGGAAGCTAT 2100

Db 2041 TGTAATTGAATATTATTCTCCCAAAAATTCACATAGTAGAACGCTATCTGGGAAGCTAT 2100

QY 2101 TTTTTTTCAGTTTGTGATATTTTCTAGCTTATCTACTTCCAAACTAATTTTTTTTGTCTGA 2160

Db 2101 TTTTTTTCAGTTTGTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTTTTTGTCTGA 2160

QY 2161 GACTAATCTTATTCTATTTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAAAC 2220

Db 2161 GACTAATCTTATTCTATTTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAAAC 2220

QY 2221 ATACTAAGAAGTACATTGTGTACCTCTATATACCAAAAGCACATTTTAAAAAGTGCCATTAA 2280

Db 2221 ATACTAAGAAGTACATTGTGTACCTCTATATACCAAAAGCACATTTTAAAAAGTGCCATTAA 2280

QY 2281 CAAATGTATCACTAGCCCTCCTTTTCCAAACAAGAGGGACTGAGAGATGCAGAAATATT 2340

Db 2281 CAAATGTATCACTAGCCCTCCTTTTCCAAACAAGAGGGACTGAGAGATGCAGAAATATT 2340

QY 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372

Db 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372

RESULT 6

ABL88087
ID ABL88087 standard; cDNA; 2372 BP.
XX
AC ABL88087;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO263 cDNA sequence SEQ ID NO:31.
XX
KW Human; angiogenesis; cardiac; cytostatic; antiangiogenic; hypotensive; vulnary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.
OS Homo sapiens.
XX
PN WO200200690-A2.
XX
PD 03-JAN-2002.
XX
PF 20-JUN-2001; 2001WO-US019692.
XX
PR 23-JUN-2000; 2000US-0213637P.
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.

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PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-090516/12.
DR P-PSDB; ABB84832.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 2; Fig 31; 565pp; English.
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
Query Match 100.0%; Score 2372; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCAGGGAAATCCGGATGTCGCGTTATGAAGTGGAGCAGTGAAGTGTGAGCCTCAACATA 60
Db 1 AGCAGGGAAATCCGGATGTCGCGTTATGAAGTGGAGCAGTGAAGTGTGAGCCTCAACATA 60
QY 61 GTTCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
Db 61 GTTCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
QY 121 CATCTGAGGTGTTTCCCTCGGCTCTGAAGGGGTAGGCACGATGSCCAGGTGCTTCAGCCTG 180
Db 121 CATCTGAGGTGTTTCCCTCGGCTCTGAAGGGGTAGGCACGATGSCCAGGTGCTTCAGCCTG 180
QY 181 GTGTTGCTTCTCACTTCCATCTGGACACAGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
Db 181 GTGTTGCTTCTCACTTCCATCTGGACACAGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
QY 241 GAAGAGCTTTCATCCAGGTGTCAATGCAGAAATTATGGGGATACCCCTTGTGAGCAAAAAG 300
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Db 241 GAAGAGCTTTCATCCAGGTGTCAATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAG 300
QY 301 GCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGT 360
Db 301 GCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGT 360
QY 361 TTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAGAGCTAGCTTTGAAACCTTGCACTAT 420
Db 361 TTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAGAGCTAGCTTTGAAACCTTGCACTAT 420
QY 421 GGCTGGGTTGGAGATGGATTTCGTGGTCACTCTAGGATTAGCCCCAAACCCCAAGTGTGGG 480
Db 421 GGCTGGGTTGGAGATGGATTTCGTGGTCACTCTAGGATTAGCCCCAAACCCCAAGTGTGGG 480
QY 481 AAAAATGGGTTGGGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
Db 481 AAAAATGGGTTGGGTCCTGATTTTGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
QY 541 TGTACAACCTCATCTGATACTTGGACTAACTCGTGCAATCCAGAAATTATCACCAACAAA 600
Db 541 TGTACAACCTCATCTGATACTTGGACTAACTCGTGCAATCCAGAAATTATCACCAACAAA 600
QY 601 GATCCCATATTTCAACACTCAAACTGCAACACACAAACAGAAATTTATTGTCAGTGACAGT 660
Db 601 GATCCCATATTTCAACACTCAAACTGCAACACACAAACAGAAATTTATTGTCAGTGACAGT 660
QY 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTTACTACTACTCCTCTCTGCT 720
Db 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTTACTACTACTCCTCTCTGCT 720
QY 721 CCAGCTTCCACTTCTATTTCCACGGAGAAAAAATTGATTTGTGTACAGAAAGTTTTTATG 780
Db 721 CCAGCTTCCACTTCTATTTCCACGGAGAAAAAATTGATTTGTGTACAGAAAGTTTTTATG 780
QY 781 GAAACTAGCACCATGTCTACAGAAAACTGAACCATTTGTGAAAAATAAAGCAGCATTTCAAG 840
Db 781 GAAACTAGCACCATGTCTACAGAAAACTGAACCATTTGTGAAAAATAAAGCAGCATTTCAAG 840
QY 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCCAACGGCTCTGCTAGTGTCTCTCTCTCTTC 900
Db 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCCAACGGCTCTGCTAGTGTCTCTCTCTCTTC 900
QY 901 TTTGGTGTGCAGCTGGTCTTGGATTTTGTCTATGTCAAAAAGGTATGTGAAGGCTTCCCT 960
Db 901 TTTGGTGTGCAGCTGGTCTTGGATTTTGTCTATGTCAAAAAGGTATGTGAAGGCTTCCCT 960
QY 961 TTTACAACAAGAAATCAGCAGAAGAAATGATCGAAACCAAAAGTAGTAAAGGAGGAGAAG 1020
Db 961 TTTACAACAAGAAATCAGCAGAAGAAATGATCGAAACCAAAAGTAGTAAAGGAGGAGAAG 1020
QY 1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACTGATAAAAAACCCAGAGAGTCC 1080
Db 1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACTGATAAAAAACCCAGAGAGTCC 1080
QY 1081 AAGAGTCCAAGCAAAAACCTACCGTCCGATGCCTGGAAGCTGAAAGTTTAGATGAGACAGAAA 1140
Db 1081 AAGAGTCCAAGCAAAAACCTACCGTCCGATGCCTGGAAGCTGAAAGTTTAGATGAGACAGAAA 1140
QY 1141 TGAGGAGACACACCTGAGGCTGTTTCTTTCATGCTCCTTACCTGCCCTGAGCTGGGGAA 1200
Db 1141 TGAGGAGACACACCTGAGGCTGTTTCTTTCATGCTCCTTACCTGCCCTGAGCTGGGGAA 1200
QY 1201 ATCAAAAGGGCCAAAGAACCCAAAGAGAAAGTCCACCCCTTGTTTCTTAAGTGAATCAGC 1260
Db 1201 ATCAAAAGGGCCAAAGAACCCAAAGAGAAAGTCCACCCCTTGTTTCTTAAGTGAATCAGC 1260
QY 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1320
Db 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1320
QY 1321 CCTGTCTGGATCCTATCCTCCTACTCCTCAAAGCTTCCCACGGCTTTCTAGCCTGGCTAT 1380
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Db	1321	CCTGTCGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT	1380
QY	1381	GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTGTGCAAAGTGCAAGGACCTAAAACATC	1440
Db	1381		
Db	1381	GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTGTGCAAAGTGCAAGGACCTAAAACATC	1440
QY	1441	TCATCAGTATCCAGTGGTAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC	1500
Db	1441		
Db	1441	TCATCAGTATCCAGTGGTAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC	1500
QY	1501	CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTTCTTCA	1560
Db	1501		
Db	1501	CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTTCTTCA	1560
QY	1561	GCTCTGAAAGAGAAACACGATATCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA	1620
Db	1561		
Db	1561	GCTCTGAAAGAGAAACACGATATCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA	1620
QY	1621	AGAAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAAATTGAGACCTAA	1680
Db	1621		
Db	1621	AGAAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAAATTGAGACCTAA	1680
QY	1681	TCTCTGTAAAGCTAAAATAAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACTGTCA	1740
Db	1681		
Db	1681	TCTCTGTAAAGCTAAAATAAAGRAATAGAACAAAGGCTGAGGATACGACAGTACACTGTCA	1740
QY	1741	GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAAT	1800
Db	1741		
Db	1741	GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAAT	1800
QY	1801	CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT	1860
Db	1801		
Db	1801	CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT	1860
QY	1861	AGGAAATATACTTTTACAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT	1920
Db	1861		
Db	1861	AGGAAATATACTTTTACAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT	1920
QY	1921	GAGTTACAGAAATGATTACTTAAGGAAGATTACTCAGTAATTTGTTTAAAGTAATAAAA	1980
Db	1921		
Db	1921	GAGTTACAGAAATGATTACTTAAGGAAGATTACTCAGTAATTTGTTTAAAGTAATAAAA	1980
QY	1981	TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTC	2040
Db	1981		
Db	1981	TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTC	2040
QY	2041	TGTAATTGAATATTATTCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTAT	2100
Db	2041		
Db	2041	TGTAATTGAATATTATTCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTAT	2100
QY	2101	TTTTTTCAGTTTGTATATTCTAGCTTATCTACTTCCAACTAATTTTATTTTGTCTGA	2160
Db	2101		
Db	2101	TTTTTTCAGTTTGTATATTCTAGCTTATCTACTTCCAACTAATTTTATTTTGTCTGA	2160
QY	2161	GACTAATCTTATTCATTTTCTCTAATATGGCAACCATTAATAACCTTAATTATTATTAAC	2220
Db	2161		
Db	2161	GACTAATCTTATTCATTTTCTCTAATATGGCAACCATTAATAACCTTAATTATTATTAAC	2220
QY	2221	ATACCTAAGAAGTACATTGTTTACCTCTATATACCAAGGACATTTTAAAGTGCCATTAA	2280
Db	2221		
Db	2221	ATACCTAAGAAGTACATTGTTTACCTCTATATACCAAGGACATTTTAAAGTGCCATTAA	2280
QY	2281	CAAAATGTATCACTAGCCCTCCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAATATT	2340
Db	2281		
Db	2281	CAAAATGTATCACTAGCCCTCCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAATATT	2340
QY	2341	TGTGACAAAAAATTAAAGCATTTAGAAAACTT	2372
Db	2341		
Db	2341	TGTGACAAAAAATTAAAGCATTTAGAAAACTT	2372

ID	ABL95576	standard; cDNA; 2372 BP.
XX		
AC	ABL95576;	
XX		
DT	19-JUL-2002	(first entry)
XX		
DE	Human angiogenesis related cDNA	PRO263 SEQ ID NO: 31.
XX		
KW	Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;	
KW	atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;	
KW	cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;	
KW	antiarteriosclerotic; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200208284-A2.	
XX		
PD	31-JAN-2002.	
PF		
XX	09-JUL-2001; 2001WO-US021735.	
PR	20-JUL-2000; 2000US-0219556P.	
PR	25-JUL-2000; 2000US-0220624P.	
PR	25-JUL-2000; 2000US-0220664P.	
PR	28-JUL-2000; 2000WO-US020710.	
PR	02-AUG-2000; 2000US-0222695P.	
PR	17-AUG-2000; 2000US-00643657.	
PR	23-AUG-2000; 2000WO-US023522.	
PR	24-AUG-2000; 2000WO-US023328.	
PR	07-SEP-2000; 2000US-0230978P.	
PR	18-SEP-2000; 2000US-00664610.	
PR	18-SEP-2000; 2000US-00665350.	
PR	24-OCT-2000; 2000US-0242922P.	
PR	08-NOV-2000; 2000US-00709238.	
PR	08-NOV-2000; 2000WO-US030952.	
PR	10-NOV-2000; 2000WO-US030873.	
PR	01-DEC-2000; 2000WO-US032678.	
PR	20-DEC-2000; 2000US-00747259.	
PR	20-DEC-2000; 2000WO-US034956.	
PR	22-JAN-2001; 2001US-00767609.	
PR	28-FEB-2001; 2001US-00796498.	
PR	28-FEB-2001; 2001WO-US006520.	
PR	01-MAR-2001; 2001WO-US006666.	
PR	09-MAR-2001; 2001US-00802706.	
PR	14-MAR-2001; 2001US-00808689.	
PR	22-MAR-2001; 2001US-00816744.	
PR	05-APR-2001; 2001US-00828366.	
PR	10-MAY-2001; 2001US-00854208.	
PR	10-MAY-2001; 2001US-00854280.	
PR	25-MAY-2001; 2001US-00866028.	
PR	25-MAY-2001; 2001US-00866034.	
PR	25-MAY-2001; 2001WO-US017092.	
PR	30-MAY-2001; 2001US-00870574.	
PR	30-MAY-2001; 2001WO-US017443.	
PR	01-JUN-2001; 2001WO-US017800.	
PR	20-JUN-2001; 2001WO-US019692.	
XX		
PA	(GETH) GENENTECH INC.	
PA	(BAKE/) BAKER K P.	
PA	(FERR/) FERRARA N.	
PA	(GERB/) GERBER H.	
PA	(GERR/) GERRITSEN M E.	
PA	(GODD/) GODDARD A.	
PA	(GODO/) GODOWSKI P J.	
PA	(GURN/) GURNEY A L.	
PA	(HILL/) HILLAN K J.	
PA	(MARS/) MARSTERS S A.	
PA	(PANJ/) PAN J.	
PA	(PAON/) PAONI N F.	
PA	(STEP/) STEPHAN J F.	
PA	(WATA/) WATANABE C K.	
PA	(WILL/) WILLIAMS P M.	
PA	(WOOD/) WOOD W I.	

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2002-171999/22.
DR P-PSDB; ABB95438.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 1; Fig 31; 567pp; English.
PS
XX The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a coding sequence of the invention
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCAGGGAAATCCGGATGTCFCGGTTATGAAGTGGAGCAGTGAGTGCCTCAACATA 60
Db |||
1 AGCAGGGAAATCCGGATGTCFCGGTTATGAAGTGGAGCAGTGAGTGCCTCAACATA 60

QY 61 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGC 120
Db |||
61 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGC 120

QY 121 CATCTGAGGTGTTCCCTGGTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
Db |||
121 CATCTGAGGTGTTCCCTGGTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180

QY 181 GTGTTGCTTCTCACTTCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
Db |||
181 GTGTTGCTTCTCACTTCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240

QY 241 GAAGAGCTTTCATCCAGTGTCTATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAG 300
Db |||
241 GAAGAGCTTTCATCCAGTGTCTATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAG 300

QY 301 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCGCTGTAGGCTGTGGGACTAAGT 360
Db |||
301 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCGCTGTAGGCTGTGGGACTAAGT 360

QY 361 TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAACTTGCAGCTAT 420
Db |||
361 TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAACTTGCAGCTAT 420

QY 421 GGCTGGGTGGAGATGGATTCCGTGGTCACTCTAGGATTAGCCCAACCCCAAGTGTGGG 480
Db |||
421 GGCTGGGTGGAGATGGATTCCGTGGTCACTCTAGGATTAGCCCAACCCCAAGTGTGGG 480

QY 481 AAAAAATGGGTGGGTGTCCTGATTGGAAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
Db |||
481 AAAAAATGGGTGGGTGTCCTGATTGGAAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540

QY 541 TGTTACAACACTCATCTGATACCTTGGAATAACTCGTGCAATTCAGAAATTATCACCAACAA 600
Db |||
541 TGTTACAACACTCATCTGATACCTTGGAATAACTCGTGCAATTCAGAAATTATCACCAACAA 600

QY 601 GATCCCATATTCAACACTCAAACCTGCAACACAAACACAGAATTTATTGTGAGTGACAGT 660
Db |||
601 GATCCCATATTCAACACTCAAACCTGCAACACAAACACAGAATTTATTGTGAGTGACAGT 660

QY 661 ACCTACTCGGTGGATCCCCTTACTCTACAATACCTGCCCCCTACTACTCTCCTCTGCT 720
Db |||
661 ACCTACTCGGTGGATCCCCTTACTCTACAATACCTGCCCCCTACTACTCTCCTCTGCT 720

QY 721 CCAGCTTCCACTTCTATTCACGGAGAAAAAANTGATTTGTGTACAGAAAGTTTATG 780
Db |||
721 CCAGCTTCCACTTCTATTCACGGAGAAAAAANTGATTTGTGTACAGAAAGTTTATG 780

QY 781 GAAACTAGCACCATGTCTACAGAAACTGAACCAATTTGTTGAAAAATAAAGCAGCAATCAAG 840
Db |||
781 GAAACTAGCACCATGTCTACAGAAACTGAACCAATTTGTTGAAAAATAAAGCAGCAATCAAG 840

QY 841 AATGAAGCTGCTGGGTTGGAGGTGTCCCACGGCTCTGTAGTGTCTCCTCTTTC 900
Db |||
841 AATGAAGCTGCTGGGTTGGAGGTGTCCCACGGCTCTGTAGTGTCTCCTCTTTC 900

QY 901 TTTGGTGTGCAGCTGCTTGGATTTTGTCTATGTCAAAAAGGTATGTGAAGGCCCTTCCCT 960
Db |||
901 TTTGGTGTGCAGCTGCTTGGATTTTGTCTATGTCAAAAAGGTATGTGAAGGCCCTTCCCT 960

QY 961 TTTACAAAACAAGATCAGCAGAAAGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAAG 1020
Db |||
961 TTTACAAAACAAGATCAGCAGAAAGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAAG 1020

QY 1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACTGATAAAAACCCAGAAAGTCC 1080
Db |||
1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACTGATAAAAACCCAGAAAGTCC 1080

QY 1081 AAGAGTCCAAAGCAAACTACCGTCCGATGCCTGGAGTGAAGTTTAGATGAGACAGAAA 1140
Db |||
1081 AAGAGTCCAAAGCAAACTACCGTCCGATGCCTGGAGTGAAGTTTAGATGAGACAGAAA 1140

QY 1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGTCTTACCCCTGCCCCAGCTGGGAA 1200
Db |||
1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGTCTTACCCCTGCCCCAGCTGGGAA 1200

QY 1201 ATCAAAGGGCCAAAGAACCAAGAAAGAGTCCACCCCTTGGTTCCCTAACTGGAATCAGC 1260
Db |||
1201 ATCAAAGGGCCAAAGAACCAAGAAAGAGTCCACCCCTTGGTTCCCTAACTGGAATCAGC 1260

QY 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGATGCCCTTCTCCTTATTGTAAC 1320
Db |||
1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGATGCCCTTCTCCTTATTGTAAC 1320

QY 1321 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT 1380
Db |||
1321 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT 1380

QY 1381 GTCCCTAATAATATCCCACCTGGGAGAAAGGAGTTTTCGAAAAGTCAAGGACCTAAACATC 1440
Db |||
1381 GTCCCTAATAATATCCCACCTGGGAGAAAGGAGTTTTCGAAAAGTCAAGGACCTAAACATC 1440

QY 1441 TCATCAGTATCCAGTGGTAAAGGCTTCTCTACTGATTCCGAGCTCAGACCCCTTCTTCA 1500
Db |||
1441 TCATCAGTATCCAGTGGTAAAGGCTTCTCTACTGATTCCGAGCTCAGACCCCTTCTTCA 1500

QY 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGAGCTCAGACCCCTTCTTCA 1560
Db |||
1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGAGCTCAGACCCCTTCTTCA 1560

QY 1561 GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCCGTAAGAGCAAA 1620
Db |||
1561 GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCCGTAAGAGCAAA 1620

QY 1621 AGAATGGCAGAAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680
Db |||
1621 AGAATGGCAGAAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680

QY 1681 TCTCTGTAAGCTAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1740
Db |||
1681 TCTCTGTAAGCTAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1740

QY 1741 GCAGGACTGTAAACACACAGACAGGGTCAAAGTGTCTTCTGAAACACATTGAGTTGGAAT 1800

Db 1741 GCAGGGACTGTAAACACAGACAGAGGGTCAAAGTGTTCCTCTGAACACATTGAGTTGGAAAT 1800
QY 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860
Db 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860
QY 1861 AGGAAATATACCTTTTACAAGTAACAAAAATATAAACTCTTATAAAATTTCTATTTTATCT 1920
Db 1861 AGGAAATATACCTTTTACAAGTAACAAAAATATAAACTCTTATAAAATTTCTATTTTATCT 1920
QY 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
Db 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
QY 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTC 2040
Db 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTC 2040
QY 2041 TGTAATTGAATATTATTCCTCAAAAAATTGCCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
Db 2041 TGTAATTGAATATTATTCCTCAAAAAATTGCCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
QY 2101 TTTTTCAGTTTGGATATTCTAGCTTATCTACTTCCAACTAAATTTTATTTTGTCTGA 2160
Db 2101 TTTTTCAGTTTGGATATTCTAGCTTATCTACTTCCAACTAAATTTTATTTTGTCTGA 2160
QY 2161 GACTAATCTTATTCATTTTCTCTAATATGGCAACCATTATAAACCCTTAATTTATTTAAAC 2220
Db 2161 GACTAATCTTATTCATTTTCTCTAATATGGCAACCATTATAAACCCTTAATTTATTTAAAC 2220
QY 2221 ATACCTAAGGAAGTACATTTGTTACCTCTATATACCAAGCACATTTTAAAGTGCCATTAA 2280
Db 2221 ATACCTAAGGAAGTACATTTGTTACCTCTATATACCAAGCACATTTTAAAGTGCCATTAA 2280
QY 2281 CAAATGTATCACTAGCCCTCCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAATATT 2340
Db 2281 CAAATGTATCACTAGCCCTCCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAATATT 2340
QY 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372
Db 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372

RESULT 8
ACA59060

ID ACA59060 standard; cDNA; 2372 BP.

XX AC ACA59060;

XX AC ACA59060;

DT 16-JUN-2003 (first entry)

XX DE Human PRO polynucleotide #36.

XX KW Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide; pathological disorder; cardiac insufficiency disorder; protein secretion; pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis; skin disease; keratinocyte differentiation; epithelial cancer; tumour; lung squamous cell carcinoma; epidermoid carcinoma; vulva; glioma; cytostatic; cardiant; endocrine; antidiabetic; gastrointestinal; antiulcer; dermatological; vulnerary.

XX OS Homo sapiens.

XX PN US2002146709-A1.

XX PD 10-OCT-2002.

XX PF 18-JUL-2001; 2001US-00909088.

XX PR 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
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PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
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PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.

QY	1561	GCTCTGAAAGAGAAACACG	TATCCACCTGACATGTCTTCTGAGCCGGTAAGAGCAA	1620
Db	1561	GCTCTGAAAGAGAAACACG	TATCCACCTGACATGTCTTCTGAGCCGGTAAGAGCAA	1620
QY	1621	AGAAATGGCAGAAAAGTTT	AGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTTAA	1680
Db	1621	AGAAATGGCAGAAAAGTTT	AGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTTAA	1680
QY	1681	TCTCTGTAAAGCTAAATAA	AGAAATAGAACAAAGGCTGAGGATACGACAGTACACTGTCA	1740
Db	1681	TCTCTGTAAAGCTAAATAA	AGAAATAGAACAAAGGCTGAGGATACGACAGTACACTGTCA	1740
QY	1741	GCAGGACTGTAAACACAGA	CACAGGGTCAAAGTGTCTCTGAAACACATTGAGTTGGAA	1800
Db	1741	GCAGGACTGTAAACACAGA	CACAGGGTCAAAGTGTCTCTGAAACACATTGAGTTGGAA	1800
QY	1801	CACTGTTTAGAACACACAC	ACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1860
Db	1801	CACTGTTTAGAACACACAC	ACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1860
QY	1861	AGGAATATACTTTTACAAG	TAAACAAAAAATCTTATAAAATTTCTATTTTATCT	1920
Db	1861	AGGAATATACTTTTACAAG	TAAACAAAAAATCTTATAAAATTTCTATTTTATCT	1920
QY	1921	GAGTTACAGAAATGATTAC	TAAAGGAAGATTACTCAGTAATTGTTTAAAAAGTAATAAAA	1980
Db	1921	GAGTTACAGAAATGATTAC	TAAAGGAAGATTACTCAGTAATTGTTTAAAAAGTAATAAAA	1980
QY	1981	TTCAACAAACATTTGCTGA	ATAGCTACTATATGTCAAGTGTGCAAGGTATTACACTC	2040
Db	1981	TTCAACAAACATTTGCTGA	ATAGCTACTATATGTCAAGTGTGCAAGGTATTACACTC	2040
QY	2041	TGTAATTGAATATTATTC	CTCAAAAAATGCACATAGTAGAAGCTATCTGGGAAGCTAT	2100
Db	2041	TGTAATTGAATATTATTC	CTCAAAAAATGCACATAGTAGAAGCTATCTGGGAAGCTAT	2100
QY	2101	TTTTTTCAGTTTGGATA	TTTCTAGCTTATCTACTTCCAACTAAATTTTATTTTGTCTGA	2160
Db	2101	TTTTTTCAGTTTGGATA	TTTCTAGCTTATCTACTTCCAACTAAATTTTATTTTGTCTGA	2160
QY	2161	GACTAATCTTATTTCAT	TTTTCTTAATATGGCAACCATTTAACCCTTAATTTATTATTAA	2220
Db	2161	GACTAATCTTATTTCAT	TTTTCTTAATATGGCAACCATTTAACCCTTAATTTATTATTAA	2220
QY	2221	ATACCTAAGAAGTACATT	GTGTACCTCTATATACCAAAGCACATTTTAAAAGTGCCATTAA	2280
Db	2221	ATACCTAAGAAGTACATT	GTGTACCTCTATATACCAAAGCACATTTTAAAAGTGCCATTAA	2280
QY	2281	CAAAATGTATCACTAG	CCCTCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAATATT	2340
Db	2281	CAAAATGTATCACTAG	CCCTCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAATATT	2340
QY	2341	TGTGACAAAAAATTAA	AGCAATTTAGAAAACTT	2372
Db	2341	TGTGACAAAAAATTAA	AGCAATTTAGAAAACTT	2372

RESULT 9
ACA58457
ID ACA58457 standard; cDNA; 2372 BP.
XX
AC ACA58457;
XX
DT 10-JUN-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #36.
XX
KW Human; secreted and transmembrane protein; PRO polypeptide; cancer;
KW Alzheimer's disease; ischaemia; cytostatic; nootropic; vasotropic;
KW neuroprotective; gene; ss.
XX
OS Homo sapiens.
XX

PN	US2002192659-A1.
XX	
PD	19-DEC-2002.
XX	
PF	10-JUL-2001; 2001US-00902853.
XX	
PR	17-SEP-1997; 97US-0059113P.
PR	17-SEP-1997; 97US-0059115P.
PR	17-SEP-1997; 97US-0059117P.
PR	17-SEP-1997; 97US-0059119P.
PR	17-SEP-1997; 97US-0059121P.
PR	17-SEP-1997; 97US-0059122P.
PR	17-SEP-1997; 97US-0059184P.
PR	18-SEP-1997; 97US-0059263P.
PR	18-SEP-1997; 97US-0059266P.
PR	15-OCT-1997; 97US-0062125P.
PR	17-OCT-1997; 97US-0062285P.
PR	17-OCT-1997; 97US-0062287P.
PR	21-OCT-1997; 97US-0063486P.
PR	24-OCT-1997; 97US-0062814P.
PR	24-OCT-1997; 97US-0062816P.
PR	24-OCT-1997; 97US-0063045P.
PR	24-OCT-1997; 97US-0063120P.
PR	24-OCT-1997; 97US-0063121P.
PR	24-OCT-1997; 97US-0063127P.
PR	24-OCT-1997; 97US-0063128P.
PR	27-OCT-1997; 97US-0063327P.
PR	27-OCT-1997; 97US-0063329P.
PR	28-OCT-1997; 97US-0063541P.
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PR	28-OCT-1997; 97US-0063549P.
PR	28-OCT-1997; 97US-0063550P.
PR	28-OCT-1997; 97US-0063564P.
PR	29-OCT-1997; 97US-0063435P.
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PR	29-OCT-1997; 97US-0063738P.
PR	29-OCT-1997; 97US-0064215P.
PR	31-OCT-1997; 97US-0063870P.
PR	31-OCT-1997; 97US-0064103P.
PR	03-NOV-1997; 97US-0064248P.
PR	07-NOV-1997; 97US-0064809P.
PR	12-NOV-1997; 97US-0065186P.
PR	17-NOV-1997; 97US-0065846P.
PR	18-NOV-1997; 97US-0065693P.
PR	21-NOV-1997; 97US-0066120P.
PR	21-NOV-1997; 97US-0066364P.
PR	24-NOV-1997; 97US-0066453P.
PR	24-NOV-1997; 97US-0066466P.
PR	24-NOV-1997; 97US-0066511P.
PR	24-NOV-1997; 97US-0066770P.
PR	24-NOV-1997; 97US-0066772P.
PR	10-SEP-1998; 98WO-US018824.
PR	14-SEP-1998; 98WO-US019177.
PR	16-SEP-1998; 98WO-US019330.
PR	17-SEP-1998; 98WO-US019437.
PR	01-DEC-1998; 98WO-US025108.
PR	08-SEP-1999; 99WO-US020594.
PR	13-SEP-1999; 99WO-US020944.
PR	15-SEP-1999; 99WO-US021090.
PR	15-SEP-1999; 99WO-US021547.
PR	05-OCT-1999; 99WO-US023089.
PR	29-NOV-1999; 99WO-US028214.
PR	30-NOV-1999; 99WO-US028313.
PR	01-DEC-1999; 99WO-US028301.
PR	02-DEC-1999; 99WO-US028564.
PR	02-DEC-1999; 99WO-US028565.
PR	16-DEC-1999; 99WO-US030095.
PR	20-DEC-1999; 99WO-US030911.
PR	20-DEC-1999; 99WO-US030999.


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QY 1441 TCATCAGTATCCAGTGGTAAAGGCGCTCTGGCTGTCTGAGGTAGGTGGTTGAAAGC 1500
Db      |||||||
QY 1441 TCATCAGTATCCAGTGGTAAAGGCGCTCTGGCTGTCTGAGGTAGGTGGTTGAAAGC 1500
Db      |||||||
QY 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
Db      |||||||
QY 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
Db      |||||||
QY 1561 GCTCTGAAAGAGAAACACGATATCCGACCTGACATGTCTTCTGAGCCCGGTAAAGACAAA 1620
Db      |||||||
QY 1561 GCTCTGAAAGAGAAACACGATATCCGACCTGACATGTCTTCTGAGCCCGGTAAAGACAAA 1620
Db      |||||||
QY 1621 AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680
Db      |||||||
QY 1621 AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680
Db      |||||||
QY 1681 TCTCTGTAAAGCTAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1740
Db      |||||||
QY 1681 TCTCTGTAAAGCTAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1740
Db      |||||||
QY 1741 GCAGGACTGTAAACACAGACAGGCTCAAAAGTGTCTTCTGCTCTACCACTGCTGATATTTCTCT 1800
Db      |||||||
QY 1741 GCAGGACTGTAAACACAGACAGGCTCAAAAGTGTCTTCTGCTCTACCACTGCTGATATTTCTCT 1800
Db      |||||||
QY 1801 CACTGTTTGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCTCT 1860
Db      |||||||
QY 1801 CACTGTTTGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCTCT 1860
Db      |||||||
QY 1861 AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAAATTTCTATTTTATCT 1920
Db      |||||||
QY 1861 AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAAATTTCTATTTTATCT 1920
Db      |||||||
QY 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTTAAAAAGTAATAAAA 1980
Db      |||||||
QY 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTTAAAAAGTAATAAAA 1980
Db      |||||||
QY 1981 TTCAACAAACATTTGCTGTAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTC 2040
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QY 1981 TTCAACAAACATTTGCTGTAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTC 2040
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QY 2041 TGTAATTGAATATATTCTTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
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QY 2041 TGTAATTGAATATATTCTTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
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QY 2101 TTTTTCAGTTTGTATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTTTGTCTGA 2160
Db      |||||||
QY 2101 TTTTTCAGTTTGTATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTTTGTCTGA 2160
Db      |||||||
QY 2161 GACTAATCTTATTCATTTTCTTAATATGGCAACCATTAATTAACCTTAATTTATTAATAAC 2220
Db      |||||||
QY 2161 GACTAATCTTATTCATTTTCTTAATATGGCAACCATTAATTAACCTTAATTTATTAATAAC 2220
Db      |||||||
QY 2221 ATACCTAAGAAGTACATTGTTACCTCTATATACCAAGCACATTTTAAAAAGTGCCATTAA 2280
Db      |||||||
QY 2221 ATACCTAAGAAGTACATTGTTACCTCTATATACCAAGCACATTTTAAAAAGTGCCATTAA 2280
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QY 2281 CAAATGTATCACTAGCCCTCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAATATT 2340
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QY 2281 CAAATGTATCACTAGCCCTCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAATATT 2340
Db      |||||||
QY 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372
Db      |||||||
QY 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372
Db      |||||||
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RESULT 10
ACA60164
ID ACA60164 standard; cDNA; 2372 BP.
XX
AC ACA60164;
XX
DT 12-JUN-2003 (first entry)
XX

DE Human cDNA for secreted/transmembrane protein PRO263.
XX Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW gene therapy; chromosome identification; chromosome marker.
XX Homo sapiens.

OS
XX
PN US2003003530-A1.
PD 02-JAN-2003.
XX
PF 11-JUL-2001; 2001US-00904011.
XX
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
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PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
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PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
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PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.

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PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-329602/31.
DR P-PSDB; ABU71926.
XX
PT New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, in generating probes and in tissue typing.
XX
PS Claim 2; Fig 73; 484pp; English.
XX
CC The invention relates to an isolated nucleic acid with at least 80%
CC nucleic acid sequence identity to a nucleotide sequence encoding one of
CC 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a
CC PRO protein extracellular domain. Also included are a vector comprising
CC the PRO nucleic acid, a host cell comprising the vector, producing a PRO
CC polypeptide (by culturing the host cell for the expression of the PRO
CC polypeptide, and recovering the PRO polypeptide from the cell culture),
CC an isolated PRO polypeptide (having at least 80% sequence identity to: (
CC a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino
CC acid sequence encoded by a nucleic acid molecule deposited with an ATCC
CC number (detailed in the specification); or (c) an extracellular domain of
CC a PRO polypeptide or to a PRO polypeptide lacking its associated signal
CC peptide), a chimaeric molecule comprising a PRO polypeptide of fused to a
CC heterologous amino acid sequence, an anti-PRO antibody, detecting a
CC PRO245 or PRO1868 in a sample suspected of containing the polypeptide,
CC linking a bioactive molecule to a cell expressing a PRO245 or PRO1868 and
CC modulating at least one biological activity of a cell expressing a PRO245
CC or PRO1868. Nucleic acids which encode PRO can be used to generate either
CC transgenic animals or knock-out animals which may be used in the
CC development and screening of therapeutically useful reagents. The nucleic
CC acids may also be used in gene therapy, in chromosome identification, as
CC chromosome markers, or in generating probes. The PRO polypeptides are
CC useful as molecular markers for protein electrophoresis, and the isolated
CC nucleic acids may be used for recombinantly expressing those markers. The
CC PRO polypeptides and nucleic acids may also be used in tissue typing.
CC Anti-PRO antibodies are useful in diagnostic assays for PRO, and in
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. The present sequence encodes a PRO protein
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
Query Match 100.0%; Score 2372; DB 7; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 AGCAGGGAAATCCGATGTCTCGGTTATGAAGTCGAGCAGTGAGTGTGAGCCTCAACATA 60

QY

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QY 61 GTTCCAGAACTCTCCATCCGACTAGTTATTAGCATCTGCCTCTCATATCACCAGTGGC 120
Db 61 GTTCCAGAACTCTCCATCCGACTAGTTATTAGCATCTGCCTCTCATATCACCAGTGGC 120
QY 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTCTTCAGCCTG 180
Db 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTCTTCAGCCTG 180
QY 181 GTGTTGCTTCTCACTTCCATCTGGACCAAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
Db 181 GTGTTGCTTCTCACTTCCATCTGGACCAAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
QY 241 GAAGAGCTTTCCATCCAGGTGTATGCGAATTTATGGGATCACCCCTTGTGAGCAAAAAG 300
Db 241 GAAGAGCTTTCCATCCAGGTGTATGCGAATTTATGGGATCACCCCTTGTGAGCAAAAAG 300
QY 301 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCTGTAGGCTGTGGGACTAAGT 360
Db 301 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCTGTAGGCTGTGGGACTAAGT 360
QY 361 TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420
Db 361 TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420
QY 421 GGCTGGGTTGGAGATGGATTCGTGGTCACTCTCTAGGATTAGCCCAACCCCAAGTGTGG 480
Db 421 GGCTGGGTTGGAGATGGATTCGTGGTCACTCTCTAGGATTAGCCCAACCCCAAGTGTGG 480
QY 481 AAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
Db 481 AAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
QY 541 TGTACAAACTCATCTGATACTTGGACTAACTCGTGCAATCCAGAAATATCACCACCAA 600
Db 541 TGTACAAACTCATCTGATACTTGGACTAACTCGTGCAATCCAGAAATATCACCACCAA 600
QY 601 GATCCCATATTCAACACTCAAACTGCAACACAAACACAGAAATTTATGTGAGTACAGT 660
Db 601 GATCCCATATTCAACACTCAAACTGCAACACAAACACAGAAATTTATGTGAGTACAGT 660
QY 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTCTCCTCTGCT 720
Db 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTCTCCTCTGCT 720
QY 721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGATTGTGTCACAGAAAGTTTATG 780
Db 721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGATTGTGTCACAGAAAGTTTATG 780
QY 781 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAATAAAGCAGCATTTCAAG 840
Db 781 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAATAAAGCAGCATTTCAAG 840
QY 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCCGACGGCTCTGCTAGTGTCTCTCTCTTC 900
Db 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCCGACGGCTCTGCTAGTGTCTCTCTCTTC 900
QY 901 TTTGGTGTGCAGCTGGTCTTGGATTGCTATGTCAAAGGTATGTGAAGGCTTCCCT 960
Db 901 TTTGGTGTGCAGCTGGTCTTGGATTGCTATGTCAAAGGTATGTGAAGGCTTCCCT 960
QY 961 TTTACAAACAAGAATCAGCAGAGGAATGATCGAAACCAAGTAGTAAAGGAGGAGAAG 1020
Db 961 TTTACAAACAAGAATCAGCAGAGGAATGATCGAAACCAAGTAGTAAAGGAGGAGAAG 1020
QY 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAAGAAAACTGATAAAACCCAGAGAGTCC 1080
Db 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAAGAAAACTGATAAAACCCAGAGAGTCC 1080
QY 1081 AAGAGTCCAGCAAAACTACCGTCCGATCCCTGGAGCTGAAGTTTAGATGAGACAGAAA 1140
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Db 1081 AAGAGTCCAAGCAAAACTACCGTGCATGCTCGAAGCTGAAGTTAGATGAGACAGAAA 1140

QY 1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCTGCCCCAGCTGGGAA 1200

Db 1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCTGCCCCAGCTGGGAA 1200

QY 1201 ATCAAAAGGGCCAAAGAACCAAGAAGAAAGTCCACCCCTTGGTTCCTAACTGGAATCAGC 1260

Db 1201 ATCAAAAGGGCCAAAGAACCAAGAAGAAAGTCCACCCCTTGGTTCCTAACTGGAATCAGC 1260

QY 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1320

Db 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1320

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Db 1321 CCTGCTCGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCTTCTAGCCTGGCTAT 1380

QY 1381 GTCCTAATAATATCCCACCTGGGAGAAAGGAGTTTTCGAAAGTGCAGGACCTAAAAATC 1440

Db 1381 GTCCTAATAATATCCCACCTGGGAGAAAGGAGTTTTCGAAAGTGCAGGACCTAAAAATC 1440

QY 1441 TCATCAGTATCCAGTGTAAAAAGGCCCTCCTGGCTGTCTGAGCTAGGTGGTTGAAAGC 1500

Db 1441 TCATCAGTATCCAGTGTAAAAAGGCCCTCCTGGCTGTCTGAGCTAGGTGGTTGAAAGC 1500

QY 1501 CAAGGAGTCACTGAGACCAAGGTTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560

Db 1501 CAAGGAGTCACTGAGACCAAGGTTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560

QY 1561 GCTCTGAAAGAGAAAACACGATATCCACCTGACATGTCTGAGCCCGGTAAGAGCAAA 1620

Db 1561 GCTCTGAAAGAGAAAACACGATATCCACCTGACATGTCTGAGCCCGGTAAGAGCAAA 1620

QY 1621 AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAAAGCTTGAGACCTAA 1680

Db 1621 AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAAAGCTTGAGACCTAA 1680

QY 1681 TCTCTGTAAAGCTAAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA 1740

Db 1681 TCTCTGTAAAGCTAAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA 1740

QY 1741 GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAAT 1800

Db 1741 GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAAT 1800

QY 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860

Db 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860

QY 1861 AGGAAATATACTTTTACAGTAACAAAAATAAAAACTCTTATAAAATTTCTATTTTATCT 1920

Db 1861 AGGAAATATACTTTTACAGTAACAAAAATAAAAACTCTTATAAAATTTCTATTTTATCT 1920

QY 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980

Db 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980

QY 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTC 2040

Db 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTC 2040

QY 2041 TGTAATTGAATATTATTCCTCAAAAAATTGCACATAGTAGAAGCTATCTGGGAAGCTAT 2100

Db 2041 TGTAATTGAATATTATTCCTCAAAAAATTGCACATAGTAGAAGCTATCTGGGAAGCTAT 2100

QY 2101 TTTTTCAGTTTGTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTTTGTCTGA 2160

Db 2101 TTTTTCAGTTTGTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTTTGTCTGA 2160

QY 2161 GACTAATCTTATTTCTCTAATATGGCAACCACTTAATTTATTTATTTAATTAAC 2220

Db 2161 GACTAATCTTATTTCTCTAATATGGCAACCACTTAATTTATTTATTTAATTAAC 2220

QY 2221 ATACCTAAGAAAGTACATTGTTACCTCTATATACCAAAAGCAATTTAAAAAGTGCCATTAA 2280

Db 2221 ATACCTAAGAAAGTACATTGTTACCTCTATATACCAAAAGCAATTTAAAAAGTGCCATTAA 2280

QY 2281 CAAATGTATCACTAGCCCTCCTTTTCCAAAGGAGGACTGAGAGATGCAGAAATATT 2340

Db 2281 CAAATGTATCACTAGCCCTCCTTTTCCAAAGGAGGACTGAGAGATGCAGAAATATT 2340

QY 2341 TGTGACAAAAAATTAAAGCAATTAGAAAACTT 2372

Db 2341 TGTGACAAAAAATTAAAGCAATTAGAAAACTT 2372

RESULT 11

ACD07564

ID ACD07564 standard; cDNA; 2372 BP.

XX

AC ACD07564;

XX

DT 07-AUG-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO263 cDNA.

XX

KW Human; secreted and transmembrane protein; PRO; pharmaceutical; diagnostic; biosensor; bioreactor; Parkinson's disease;

KW Alzheimer's disease; inflammation; nephritis; wound healing;

KW nerve repair; collateral blood vessel formation; cancer;

KW colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;

KW cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;

KW scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;

KW infertility; gene therapy; gene; ss.

XX

OS Homo sapiens.

XX

PN US2002197671-A1.

XX

PD 26-DEC-2002.

XX

PF 17-JUL-2001; 2001US-00907824.

XX

PR 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

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PR 17-SEP-1997; 97US-0059122P.

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PR 18-SEP-1997; 97US-0059263P.

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PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 24-OCT-1997; 97US-0063127P.

PR 24-OCT-1997; 97US-0063128P.

PR 27-OCT-1997; 97US-0063327P.

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PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
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PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
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PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
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PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
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PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
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PR 02-MAR-2000; 2000WO-US005841.
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PR 22-MAY-2000; 2000WO-US014042.
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PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-370793/35.
DR P-PSDB; ABO01809.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO245 or
PT PRO335), useful for treating or diagnosing e.g. Alzheimer's disease,
PT cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia
PT or strokes.
XX Claim 2; Fig 73; 482pp; English.
PS
XX The invention describes a new isolated nucleic acid molecule comprising
CC the full length coding sequence of the DNA deposited with the American
CC Type Culture Collection (e.g. ATCC Deposit No. 209258), or a sequence
CC with at least 80% identity to a DNA encoding a PRO polypeptide comprising
CC any of 61 sequences having 164-1119 amino acids fully defined in the
CC specification. The PRO polypeptides or polynucleotides are useful as
CC pharmaceuticals, diagnostics, biosensors or bioreactors. These are

CC particularly useful for detecting or treating e.g. Parkinson's disease,
CC Alzheimer's disease, inflammations, nephritis, wound healing, nerve
CC repair, collateral blood vessel formation, cancers (e.g. colorectal
CC cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid
CC arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs,
CC restenosis, dermal fibrotic conditions (e.g. keloids or scarring),
CC ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or
CC infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
CC pigs, goats, or rabbits) The PRO polypeptides are useful as targets for
CC therapeutic intervention in these diseases, and diagnostic determination
CC of the presence of these diseases. The PRO polypeptides are also useful
CC as molecular weight markers, or for chromosome identification. The PRO
CC genes are useful as hybridisation probes, or for screening libraries of
CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
CC therapy, particularly for replacing a defective gene. This sequence
CC encodes a novel human secreted and transmembrane PRO polypeptide
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 7; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCAGGAAATCCGGATGTCGGTTATGAAGTGGAGCACTGAGTGTGAGCCTCAACATA 60
|||
Db 1 AGCAGGAAATCCGGATGTCGGTTATGAAGTGGAGCACTGAGTGTGAGCCTCAACATA 60
|||

Qy 61 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
|||
Db 61 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
|||

Qy 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACATGGCCAGGTCTTACGCCTG 180
|||
Db 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACATGGCCAGGTCTTACGCCTG 180
|||

Qy 181 GTGTTGCTTCTCACTTCCATCCAGGTCTGAGGACACGAGGCTCCTGGTCCAAAGGCTCTTTCGCTGCA 240
|||
Db 181 GTGTTGCTTCTCACTTCCATCCAGGTCTGAGGACACGAGGCTCCTGGTCCAAAGGCTCTTTCGCTGCA 240
|||

Qy 241 GAAGAGCTTTCCATCCAGGTCTCATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAG 300
|||
Db 241 GAAGAGCTTTCCATCCAGGTCTCATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAG 300
|||

Qy 301 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGT 360
|||
Db 301 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGT 360
|||

Qy 361 TTGGCCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420
|||
Db 361 TTGGCCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420
|||

Qy 421 GGCTGGGTGGAGATGGATTGCTGGTCACTCTAGGATAGCCCAACCCCAAGTGTGGG 480
|||
Db 421 GGCTGGGTGGAGATGGATTGCTGGTCACTCTAGGATAGCCCAACCCCAAGTGTGGG 480
|||

Qy 481 AAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
|||
Db 481 AAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
|||

Qy 541 TGTACAACTCATCTGATCTGGACTAACTCGTGCTATCCAGAAATTATCACCACCAA 600
|||
Db 541 TGTACAACTCATCTGATCTGGACTAACTCGTGCTATCCAGAAATTATCACCACCAA 600
|||

Qy 601 GATCCCATATTCAACACTCAAACCTCAACACAAACACAAACACAGATTATTGTGAGTGACAGT 660
|||
Db 601 GATCCCATATTCAACACTCAAACCTCAACACAAACACAAACACAGATTATTGTGAGTGACAGT 660
|||

Qy 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTACTCCTCCTGCT 720
|||
Db 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTACTCCTCCTGCT 720
|||

Qy 721 CCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATTGTGTACAGAAATTTTATG 780
|||

XX Disclosure; Fig 5; 345pp; English.

PS The invention describes an antibody that specifically binds to a PRO

XX polypeptide having a fully defined amino acid sequence given in the

CC specification. The antibody is useful in identifying PRO polypeptides

CC useful for various industrial applications, including pharmaceuticals,

CC diagnostics, biosensors and bioreactors. The antibody is also used for

CC affinity purification of PRO polypeptides from recombinant cell culture

CC or natural sources. The antibody, PRO polypeptide, or its agonists or

CC antagonists, may be used for preparing a medicament for diagnosing or

CC treating a condition responsive to the antibody, PRO polypeptide, or its

CC agonists or antagonists. This sequence encodes a novel human secreted and

XX transmembrane PRO polypeptide

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 7; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCAGGGAATCCGGATGTCCTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60

DB 1 AGCAGGGAATCCGGATGTCCTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60

QY 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGC 120

DB 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGC 120

QY 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180

DB 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180

QY 181 GTGTGCTTCTCACTTCCATCTGGACACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240

DB 181 GTGTGCTTCTCACTTCCATCTGGACACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240

QY 241 GAAGAGCTTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAG 300

DB 241 GAAGAGCTTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAG 300

QY 301 GCGAACACAGCAGCTGAATTTTCAGAAAGCTAAGGAGGCTGTAGGCTGCTGGACTAAGT 360

DB 301 GCGAACACAGCAGCTGAATTTTCAGAAAGCTAAGGAGGCTGTAGGCTGCTGGACTAAGT 360

QY 361 TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTAT 420

DB 361 TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTAT 420

QY 421 GGCTGGGTGGAGATGGATTGCTGGTTCATCTCTAGGATTAGCCAAACCCCAAGTGTGG 480

DB 421 GGCTGGGTGGAGATGGATTGCTGGTTCATCTCTAGGATTAGCCAAACCCCAAGTGTGG 480

QY 481 AAAAATGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540

DB 481 AAAAATGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540

QY 541 TGTTACAACTCATCTGATCTTGGACTAACTCGTGCAATCCAGAAATTATCCACCACAAA 600

DB 541 TGTTACAACTCATCTGATCTTGGACTAACTCGTGCAATCCAGAAATTATCCACCACAAA 600

QY 601 GATCCCATATTCAACACTCAAACCTGCAACACAAAACAGAAATTATTGTCAGTGACAGT 660

DB 601 GATCCCATATTCAACACTCAAACCTGCAACACAAAACAGAAATTATTGTCAGTGACAGT 660

QY 661 ACCTACTCGGTGGCATCCCCTTACTCTACAATACTGCCCCCTACTACTCCTCCTGCT 720

DB 661 ACCTACTCGGTGGCATCCCCTTACTCTACAATACTGCCCCCTACTACTCCTCCTGCT 720

QY 721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAAGTTTTTATG 780

DB 721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAAGTTTTTATG 780

QY 781 GAAACTAGCACCATTGCTACAGAAACTGAACCATTTTGTGAAAAATAAAGCAGCATTTCAAG 840

DB 781 GAAACTAGCACCATTGCTACAGAAACTGAACCATTTTGTGAAAAATAAAGCAGCATTTCAAG 840

QY 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTGCTTCTCTCTTC 900

DB 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTGCTTCTCTCTTC 900

QY 901 TTTGGTGTGCTGAGCTGCTTGGATTTTGTATGTCAAAAAGGTATGTGAAGCCTTCCCT 960

DB 901 TTTGGTGTGCTGAGCTGCTTGGATTTTGTATGTCAAAAAGGTATGTGAAGCCTTCCCT 960

QY 961 TTTACAAAACAAGAAATCAGCAGAAAGAAATGATCGAAAAACCAAAAGTAGTAAAGGAGGAAAG 1020

DB 961 TTTACAAAACAAGAAATCAGCAGAAAGAAATGATCGAAAAACCAAAAGTAGTAAAGGAGGAAAG 1020

QY 1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACTGATAAAAAACCCAGAAAGTCC 1080

DB 1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACTGATAAAAAACCCAGAAAGTCC 1080

QY 1081 AAGAGTCCAAGCAAAACTACCGTGCATGCCCTGGAAGCTTGAAGTTTAGATGAGACAGAAA 1140

DB 1081 AAGAGTCCAAGCAAAACTACCGTGCATGCCCTGGAAGCTTGAAGTTTAGATGAGACAGAAA 1140

QY 1141 TGAGGAGACACACTGAGGCTGGTTTCTTTCTCATGCTCTTACCTGCCCCAGCTGGGGAA 1200

DB 1141 TGAGGAGACACACTGAGGCTGGTTTCTTTCTCATGCTCTTACCTGCCCCAGCTGGGGAA 1200

QY 1201 ATCAAAAGGGCCAAAGAACCAAAAGAAAGTCCACCCCTTGGTTCTTAACTGGAATCAGC 1260

DB 1201 ATCAAAAGGGCCAAAGAACCAAAAGAAAGTCCACCCCTTGGTTCTTAACTGGAATCAGC 1260

QY 1261 TCAGGACTGCCATTGGACTATGGAGTGACCAAAAGAGATGCCCTTCTCTTATTGTAAAC 1320

DB 1261 TCAGGACTGCCATTGGACTATGGAGTGACCAAAAGAGATGCCCTTCTCTTATTGTAAAC 1320

QY 1321 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCTTCTAGCCTGGCTAT 1380

DB 1321 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCTTCTAGCCTGGCTAT 1380

QY 1381 GTCTTAATAATATCCCATGGGAGAAAGGAGTTTGTGCAAGTGCAAGGACCTTAAACATC 1440

DB 1381 GTCTTAATAATATCCCATGGGAGAAAGGAGTTTGTGCAAGTGCAAGGACCTTAAACATC 1440

QY 1441 TCATCAGTATCCAGTGGTAAAAAGGCTCCTGGCTGTCTGAGGTAGGTGGTTGAAAAGC 1500

DB 1441 TCATCAGTATCCAGTGGTAAAAAGGCTCCTGGCTGTCTGAGGTAGGTGGTTGAAAAGC 1500

QY 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560

DB 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560

QY 1561 GCTCTGAAAGAGAAACACGATCCCACTGACATGTCTCTGAGCCCGGTAAAGCAAA 1620

DB 1561 GCTCTGAAAGAGAAACACGATCCCACTGACATGTCTCTGAGCCCGGTAAAGCAAA 1620

QY 1621 AGAATGGCAGAAAAAGTTTAGCCCTGAAAAAGCCATGGAGATTCATAACTTGAGACCTAA 1680

DB 1621 AGAATGGCAGAAAAAGTTTAGCCCTGAAAAAGCCATGGAGATTCATAACTTGAGACCTAA 1680

QY 1681 TCTCTGTAAGCTAAAAATAAGAAATAGAACCAAGCTGAGGATACGACAGTACACTGTCA 1740

DB 1681 TCTCTGTAAGCTAAAAATAAGAAATAGAACCAAGCTGAGGATACGACAGTACACTGTCA 1740

QY 1741 GCAGGGACTGTAAAAACACAGACAGGTCAAAAAGTGTCTCTGAAACATTTGAGTTGGAAT 1800

DB 1741 GCAGGGACTGTAAAAACACAGACAGGTCAAAAAGTGTCTCTGAAACATTTGAGTTGGAAT 1800

QY 1801 CACTGTTTAGAAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860

DB 1801 CACTGTTTAGAAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860

QY 1861 AGGAAATATACTTTTACAAGTAACAAAAATAAAAAACTCTTATAAAATTTCTATTTTATCT 1920


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Db      1861  |||||TACTTTTACAAAGTAACAAAAATAAAAATCTTTATAAAATTTCTATTTTATCT 1920
QY      1921  GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
Db      1921  GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
QY      1981  TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTC 2040
Db      1981  TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTC 2040
QY      2041  TGTAATTGAATATTATTTCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
Db      2041  TGTAATTGAATATTATTTCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
QY      2101  TTTTTCAGTTTGTGATATTTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTTGCTGA 2160
Db      2101  TTTTTCAGTTTGTGATATTTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTTGCTGA 2160
QY      2161  GACTAATCTTATTTCATTTTCTCTAAATATGGCAACCATTTAACTTAAATTTATTATTAAC 2220
Db      2161  GACTAATCTTATTTCATTTTCTCTAAATATGGCAACCATTTAACTTAAATTTATTATTAAC 2220
QY      2221  ATACCTAAGAAGTACATTGTTACCTCTATATATACCAAGCAATTTTAAAAAGTGCCATTAA 2280
Db      2221  ATACCTAAGAAGTACATTGTTACCTCTATATATACCAAGCAATTTTAAAAAGTGCCATTAA 2280
QY      2281  CAAATGTATCACTAGCCCTCCCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAATATT 2340
Db      2281  CAAATGTATCACTAGCCCTCCCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAATATT 2340
QY      2341  TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372
Db      2341  TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372
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RESULT 13

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ACD81543
ID      ACD81543 standard; cdNA; 2372 BP.
XX      AC      ACD81543;
XX      DT      18-SEP-2003 (first entry)
XX      DE      Human cDNA encoding secreted/transmembrane protein PRO263.
XX      KW      Human; ss; gene; secreted/transmembrane protein; PRO; tumour; cancer;
XX      KW      cytostatic.
XX      OS      Homo sapiens.
XX      PN      US2003009013-A1.
XX      PD      09-JAN-2003.
XX      PF      01-MAY-2002; 2002US-00063519.
XX      PR      30-DEC-1998; 98KR-00062142.
PR      08-MAR-1999; 99WO-US005028.
PR      14-MAY-1999; 99US-00311832.
PR      14-MAY-1999; 99WO-US010733.
PR      25-AUG-1999; 99US-00380137.
PR      25-AUG-1999; 99US-00380138.
PR      25-AUG-1999; 99US-00380139.
PR      25-AUG-1999; 99US-00380142.
PR      15-SEP-1999; 99US-00397342.
PR      18-OCT-1999; 99US-00403297.
PR      12-NOV-1999; 99US-00423844.
PR      30-DEC-1999; 99WO-US031274.
PR      18-FEB-2000; 2000WO-US004341.
PR      01-MAR-2000; 2000WO-US005601.
PR      02-MAR-2000; 2000WO-US005841.
PR      21-MAR-2000; 2000WO-US007532.
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PR      22-MAY-2000; 2000WO-US014042.
PR      02-JUN-2000; 2000WO-US015264.
PR      22-AUG-2000; 2000US-00644848.
PR      24-AUG-2000; 2000WO-US023328.
PR      18-SEP-2000; 2000US-00664610.
PR      18-SEP-2000; 2000US-00665350.
PR      08-NOV-2000; 2000US-00709238.
PR      10-NOV-2000; 2000WO-US030873.
PR      01-DEC-2000; 2000WO-US032678.
PR      20-DEC-2000; 2000US-00747259.
PR      20-DEC-2000; 2000WO-US034956.
PR      28-FEB-2001; 2001WO-US006520.
PR      22-MAR-2001; 2001US-00816744.
PR      10-MAY-2001; 2001US-00854208.
PR      10-MAY-2001; 2001US-00854280.
PR      30-MAY-2001; 2001US-00870574.
PR      01-JUN-2001; 2001WO-US017800.
PR      05-JUN-2001; 2001US-00874503.
PR      29-JUN-2001; 2001US-00869599.
PR      18-JUL-2001; 2001US-00908827.
PR      06-DEC-2001; 2001US-00006867.
XX
(GETH ) GENENTECH INC.
PA
XX
XX
PI      Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI      Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR      WPI; 2003-447384/42.
DR      P-PSDB; ABO33937.
XX
PT      New isolated antibody specifically binding a PRO polypeptide, useful for
PT      the preparation of a medicament for treating disorders with the aberrant
PT      expression or activity of the PRO polypeptide, such as tumor conditions
PT      and cancer.
XX
PS      Disclosure; Fig 5; 223pp; English.
XX
CC      The invention relates to an antibody that binds to a secreted or
CC      transmembrane protein designated PRO1446 appearing as ABO33941. The
CC      protein is one of 84 PRO polypeptides which (along with their encoding
CC      nucleic acids) are disclosed in the specification. The methods and
CC      compositions of the present invention are useful for the preparation of a
CC      medicament for the treatment of disorders associated with the aberrant
CC      expression or activity of the PRO polypeptide, such as tumour conditions
CC      and cancer. They can also be used to generate transgenic or knockout
CC      animals useful in the development and screening of therapeutically useful
CC      reagents. The PRO polypeptides and encoding nucleic acids can be used as
CC      molecular weight markers for protein electrophoresis, chromosome
CC      identification and tissue typing. The antibodies may be used in various
CC      diagnostic, competitive binding and/or immunoprecipitation assays. The
CC      present sequence encodes a PRO polypeptide
XX
SQ      Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
```

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Query Match      100.0%; Score 2372; DB 7; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 AGCAGGGAATCCGGATGTCGGTTATGAAGTGAGCAGTGAGTGTGAGCCTCAACATA 60
Db      1 AGCAGGGAATCCGGATGTCGGTTATGAAGTGAGCAGTGAGTGTGAGCCTCAACATA 60
QY      61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
Db      61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
QY      121 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
Db      121 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
QY      181 GTGTTGCTTCTCACTTCCATCTGGACCACGAGGTCCTGGTCCAAGGCTCTTTCGGTGCA 240
Db      181 GTGTTGCTTCTCACTTCCATCTGGACCACGAGGTCCTGGTCCAAGGCTCTTTCGGTGCA 240
```

QY	241	GAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAG	300
Db	241		
QY	301	GCGAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGT	360
Db	301		
QY	361	TTGGCCGGCAAGGACCAAGTTGAAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	420
Db	361		
QY	421	GGCTGGGTTGGAGATGGATTCGTGGTTCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGG	480
Db	421		
QY	481	AAAAATGGGTGGGTGTCCTGATTTGGAAGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	540
Db	481		
QY	541	TGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATTCAGAAATTATCACCCACAAA	600
Db	541		
QY	601	GATCCCATATTTCAACACTCAAACTGCAACACAAACAACAGAAATTTATTGTCAGTGACAGT	660
Db	601		
QY	661	ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTCTCCTCGCT	720
Db	661	ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTCTCCTCGCT	720
QY	721	CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAAGTTTTTATG	780
Db	721	CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAAGTTTTTATG	780
QY	781	GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTGAAAAATAAGCAGCATTTCAAG	840
Db	781	GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTGAAAAATAAGCAGCATTTCAAG	840
QY	841	AATGAAGCTGCTGGGTTTGGAGTGTCCCCACGGCTCTGCTAGTGCTTGCTCTCCTCTTC	900
Db	841	AATGAAGCTGCTGGGTTTGGAGTGTCCCCACGGCTCTGCTAGTGCTTGCTCTCCTCTTC	900
QY	901	TTTGGTGTGCAGCTGGTCTTGGAATTTTGCTATGTCAAAAGGTATGTGAAGGCCCTTCCCT	960
Db	901	TTTGGTGTGCAGCTGGTCTTGGAATTTTGCTATGTCAAAAGGTATGTGAAGGCCCTTCCCT	960
QY	961	TTTACAAAACAAGAATCAGCAGAAAGGAAATGATCGAAAACCAAGTAGTAAAGGAGGAGAG	1020
Db	961	TTTACAAAACAAGAATCAGCAGAAAGGAAATGATCGAAAACCAAGTAGTAAAGGAGGAGAG	1020
QY	1021	GCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAACTGATPAAAAACCCAGAAGATCC	1080
Db	1021	GCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAACTGATPAAAAACCCAGAAGATCC	1080
QY	1081	AAGAGTCCAAGCAAAAACCTACCGTGGGATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAA	1140
Db	1081	AAGAGTCCAAGCAAAAACCTACCGTGGGATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAA	1140
QY	1141	TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCTGCCCCAGCTGGGGAA	1200
Db	1141	TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCTGCCCCAGCTGGGGAA	1200
QY	1201	ATCAAAAGGGCCAAAGAACCAAGAAGAAAGTCCACCCCTTGTTCTTAACCTTAATCGAC	1260
Db	1201	ATCAAAAGGGCCAAAGAACCAAGAAGAAAGTCCACCCCTTGTTCTTAACCTTAATCGAC	1260
QY	1261	TCAGGACTGCCAATTGGACTATGGAGTGCACCAAGAGAATGCCCTTCTCCTTATTGTAAAC	1320
Db	1261	TCAGGACTGCCAATTGGACTATGGAGTGCACCAAGAGAATGCCCTTCTCCTTATTGTAAAC	1320

QY	1321	CCTGTCTGGATCCTATCCTCTCTACCTCCAAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT	1380
Db	1321		
QY	1381	GTCTCTAATAATATCCACTGGGAGAAAAGGAGTTTTTGAAAAGTCAAGGACCTTAAACATC	1440
Db	1381	GTCTCTAATAATATCCACTGGGAGAAAAGGAGTTTTTGAAAAGTCAAGGACCTTAAACATC	1440
QY	1441	TCATCAGTATCCAGTGTGTAFAAAAAGGCCTCCTGGTGTCTGAGGCTAGGTGGTTGAAAGC	1500
Db	1441	TCATCAGTATCCAGTGTGTAFAAAAAGGCCTCCTGGTGTCTGAGGCTAGGTGGTTGAAAGC	1500
QY	1501	CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTTTCTTCA	1560
Db	1501	CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTTTCTTCA	1560
QY	1561	GCTCTGAAAGAGAAAACAGTATCCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA	1620
Db	1561	GCTCTGAAAGAGAAAACAGTATCCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA	1620
QY	1621	AGAATGGCAGAAAAGTTTTAGCCCCCTGAAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1680
Db	1621	AGAATGGCAGAAAAGTTTTAGCCCCCTGAAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1680
QY	1681	TCTCTGTAAAGCTAAAAATAAGAAAATAGAACCAAGGCTGAGGATACGACAGTACACTGTCA	1740
Db	1681	TCTCTGTAAAGCTAAAAATAAGAAAATAGAACCAAGGCTGAGGATACGACAGTACACTGTCA	1740
QY	1741	GCAGGGACTGTAAACACACAGACAGGGTCAAAGTGTCTCTCTGAAACACATTGAGTTGGAAT	1800
Db	1741	GCAGGGACTGTAAACACACAGACAGGGTCAAAGTGTCTCTCTGAAACACATTGAGTTGGAAT	1800
QY	1801	CAGTGTTTAGAACACACACACTTACTTTTCTGCTCTCTACCACTGCTGATATTTTCTCT	1860
Db	1801	CAGTGTTTAGAACACACACACTTACTTTTCTGCTCTCTACCACTGCTGATATTTTCTCT	1860
QY	1861	AGGAAATATACTTTTACAAGTAAACAAAATAAAACTCTTATAAATTTTCTATTTTATCT	1920
Db	1861	AGGAAATATACTTTTACAAGTAAACAAAATAAAACTCTTATAAATTTTCTATTTTATCT	1920
QY	1921	GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA	1980
Db	1921	GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA	1980
QY	1981	TTCAACAAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTC	2040
Db	1981	TTCAACAAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTC	2040
QY	2041	TGTAATGAATATTATTCCTCAAAAAAATGCACATAGTAGAACGCTATCTGGGAAGCTAT	2100
Db	2041	TGTAATGAATATTATTCCTCAAAAAAATGCACATAGTAGAACGCTATCTGGGAAGCTAT	2100
QY	2101	TTTTTTTCAGTTTGTGATATTTCTTAGCTTATCTACTTCCAAACTAATTTTATTTTGTGA	2160
Db	2101	TTTTTTTCAGTTTGTGATATTTCTTAGCTTATCTACTTCCAAACTAATTTTATTTTGTGA	2160
QY	2161	GACTAATCTTTATTTCTTAATATGGCAACCATTTATAACCTTAATTTATTTATTTAAC	2220
Db	2161	GACTAATCTTTATTTCTTAATATGGCAACCATTTATAACCTTAATTTATTTATTTAAC	2220
QY	2221	ATACCTAAGAAGTACATTGTTTACCTCTATATACCAAGACATTTTAAAAAGTGCCATTAA	2280
Db	2221	ATACCTAAGAAGTACATTGTTTACCTCTATATACCAAGACATTTTAAAAAGTGCCATTAA	2280
QY	2281	CAAAATGTATCACTAGCCCTCCTTTTTCCAAACAAGAGGAGCTGAGAGATGCAGAAAATATT	2340
Db	2281	CAAAATGTATCACTAGCCCTCCTTTTTCCAAACAAGAGGAGCTGAGAGATGCAGAAAATATT	2340
QY	2341	TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372	
Db	2341	TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372	

RESULT 14	
ACA60365	
ID	ACA60365 standard; cDNA; 2372 BP.
XX	
AC	ACA60365;
XX	
DT	11-JUN-2003 (first entry)
XX	
DE	Novel human secreted and transmembrane protein PRO263 cDNA.
XX	
KW	Human; secreted and transmembrane polypeptide; gene;
KW	ss. chromosome mapping; gene mapping; transgenic animal; knockout animal;
KW	therapeutic agent screening; chromosome identification; tissue typing;
KW	gene therapy.
XX	
OS	Homo sapiens.
XX	
PN	US2003018183-A1.
XX	
PD	23-JAN-2003.
XX	
PF	01-MAY-2002; 2002US-00063512.
XX	
PR	06-DEC-2001; 2001US-00006867.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI	Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX	
DR	WPI; 2003-330984/31.
DR	P-PSDB; ABU71954.
XX	
PT	New secreted and transmembrane PRO polypeptides and nucleic acid
PT	molecules encoding the polypeptides, useful in gene therapy or preparing
PT	a medicament for treating a condition that is responsive to the PRO
PT	polypeptide or antibody.
XX	
PS	Disclosure; Fig 5; 409pp; English.
XX	
CC	The invention describes novel isolated PRO polypeptides. The PRO
CC	polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC	for treating a condition that is responsive to the PRO polypeptide or
CC	antibody. The PRO nucleotide sequences may be used as hybridisation
CC	probes in chromosome and gene mapping, or in generating antisense RNA and
CC	DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in
CC	assays to identify other proteins or molecules involved in binding
CC	reaction, to generate transgenic animals or knockout animals, which in
CC	turn are useful in the development and screening of therapeutically
CC	useful reagents, for chromosome identification, and tissue typing. The
CC	PRO polypeptides and nucleic acid molecules are also useful in gene
CC	therapy, and as molecular weight markers for protein electrophoresis
CC	purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC	PRO, or for the affinity purification of PRO from recombinant cell
CC	culture or natural sources. This sequence encodes a novel human secreted
CC	and transmembrane PRO polypeptide
XX	
SQ	Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
	Query Match
	Best Local Similarity 100.0%; Score 2372; DB 7; Length 2372;
	Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 AGCAGGGAAATCCGGATGTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60
Db	1 AGCAGGGAAATCCGGATGTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60
QY	61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCTCATATCACCAGTGGC 120
Db	61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCTCATATCACCAGTGGC 120
QY	121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCAGATGGCCAGGTGCTTCAGCCTG 180

QY 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCATTATTGTAAC 1320
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCATTATTGTAAC 1320
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1321 CCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT 1380
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1321 CCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT 1380
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1381 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTTGCAAAAGTCAAGGACCTAAACATC 1440
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1381 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTTGCAAAAGTCAAGGACCTAAACATC 1440
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1441 TCATCAGTATCCAGTGGTFAAAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAAGC 1500
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1441 TCATCAGTATCCAGTGGTFAAAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAAGC 1500
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1501 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGGCAGCTCAGACCCCTTTCTTCA 1560
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1501 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGGCAGCTCAGACCCCTTTCTTCA 1560
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1561 GCTCTGAAAAGAGAAAACACGTATCCCACTGACATGTCTTCTGAGCCCGGTAAGAGCAAA 1620
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1561 GCTCTGAAAAGAGAAAACACGTATCCCACTGACATGTCTTCTGAGCCCGGTAAGAGCAAA 1620
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1621 AGAATGGCAGAAAAGTTTAGCCCTGAAAAGCCATGGAGATTCTCATAAATTGAGACCTAA 1680
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1621 AGAATGGCAGAAAAGTTTAGCCCTGAAAAGCCATGGAGATTCTCATAAATTGAGACCTAA 1680
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1681 TCTCTGTAAGCTAAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1740
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1681 TCTCTGTAAGCTAAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1740
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1741 GCAGGACTGTAAACACACAGACAGGGTCAAAAGTGTCTCTGAAACACATTGAGTTGGAAT 1800
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1741 GCAGGACTGTAAACACACAGACAGGGTCAAAAGTGTCTCTGAAACACATTGAGTTGGAAT 1800
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1861 AGGAAATATACCTTTTACAAGTAACAAAATAAATAAATAAATAAATAAATAAATAAATAA 1920
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1861 AGGAAATATACCTTTTACAAGTAACAAAATAAATAAATAAATAAATAAATAAATAAATAA 1920
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTAAAAAGTAATAAAA 1980
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTAAAAAGTAATAAAA 1980
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGCAAGGTATTACACTC 2040
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGCAAGGTATTACACTC 2040
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2041 TGTAATTGAATATTATTCCTCAAAAAATTCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2041 TGTAATTGAATATTATTCCTCAAAAAATTCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2101 TTTTTCAGTTTGTGATATTCTAGCTTATCTACTTCCAAACTAATTTTATTGCTGA 2160
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2101 TTTTTCAGTTTGTGATATTCTAGCTTATCTACTTCCAAACTAATTTTATTGCTGA 2160
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2161 GACTAATCTTATTCAATTTCTCTAATATGGCAACCATTAACCTTAATTATTATTAAAC 2220
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2161 GACTAATCTTATTCAATTTCTCTAATATGGCAACCATTAACCTTAATTATTATTAAAC 2220
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2221 ATACCTAAGAAGTACATTTGTACCTCTATATACCAAGCACATTTTAAAAAGTGCCATTAA 2280
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2221 ATACCTAAGAAGTACATTTGTACCTCTATATACCAAGCACATTTTAAAAAGTGCCATTAA 2280
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2281 CAAATGTATCACTAGCCCTCCTTTTCCAAACAAGAAGGACTGAGAGATGAGAAATATT 2340
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2281 CAAATGTATCACTAGCCCTCCTTTTCCAAACAAGAAGGACTGAGAGATGAGAAATATT 2340
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
RESULT 15
ABX71612
ID ABX71612 standard; cDNA; 2372 BP.
XX
AC ABX71612;
XX
DT 10-MAR-2003 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO263.
XX
KW Human; PRO; secreted protein; transmembrane protein; enterocolitis;
KW gastrointestinal ulceration; skin disease; ss; gene;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;
KW amyotrophic lateral sclerosis; inflammatory disease;
KW rheumatoid arthritis; asthma; multiple sclerosis; organ failure;
KW atherosclerosis; cardiac injury; infertility; birth defect;
KW premature aging; AIDS; acquired immunodeficiency syndrome; cancer;
KW diabetic complication; wound repair.
XX
OS Homo sapiens.
XX
PN US2002132240-A1.
XX
PD 19-SEP-2002.
XX
PF 18-JUL-2001; 2001US-00909320.
XX
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.

PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 06-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.

(GETH) GENENTECH INC.

PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;

DR WPI; 2003-147434/14.
DR P-PSDB; ABU54382.

PT New PRO polypeptides and nucleic acid molecules, useful in diagnosing or
PT treating inflammatory diseases, organ failure, atherosclerosis, cardiac
PT injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
PT disease.

PS Claim 2; Fig 73; 473pp; English.

XX The invention relates to an isolated PRO polypeptide having at least 80%
XX amino acid sequence identity to: (a) any one of 61 fully defined amino
XX acid sequences given in the specification (appearing as ABU54347-
XX ABU54407); (b) an amino acid sequence encoded by the nucleotide sequence
XX deposited under American Type Culture Collection (accession numbers
XX listed in the specification); (c) any one of the PRO sequences which
XX lacks its associated signal peptide; (d) an extracellular domain of the
XX PRO polypeptide with its associated signal peptide; or (e) an
XX extracellular domain of the PRO polypeptide which lacks its associated
XX signal peptide. Also include are the nucleic acids encoding the PRO
XX polypeptides, vectors, host cells and anti-PRO antibodies. The PRO
XX polypeptides and nucleic acids are useful in diagnosing or treating
XX enterocolitis, gastrointestinal ulceration, skin diseases associated with
XX abnormal keratinocyte differentiation, e.g. psoriasis or epithelial
XX cancers such as squamous cell carcinoma, Alzheimer's disease, Parkinson's

CC disease, amyotrophic lateral sclerosis, inflammatory diseases, e.g.
CC rheumatoid arthritis, asthma or multiple sclerosis, organ failure,
CC atherosclerosis, cardiac injury, infertility, birth defects, premature
CC aging, AIDS, cancer, diabetic complications, or mutations in general. The
CC polypeptides are also useful for wound repair and associated therapies
CC concerned with re-growth of tissue. The nucleotide sequences may be used
CC as hybridisation probes in chromosome and gene mapping, or in generating
CC antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
CC polypeptides, in assays to identify other proteins or molecules involved
CC in binding reaction, to generate transgenic animals or knockout animals,
CC which in turn are useful in the development and screening of
CC therapeutically useful reagents, for chromosome identification, and
CC tissue typing. The PRO polypeptides and nucleic acid molecules are also
CC useful in gene therapy, and as molecular weight markers for protein
CC electrophoresis purposes. The anti-PRO antibodies may be used in
CC diagnostic assays for PRO, or for the affinity purification of PRO from
CC recombinant cell culture or natural sources. The present sequence encodes
CC a PRO polypeptide

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 7; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCAGGGAATCCGGATGTCGCGTTATGAAGTGGAGCAGTGTGAGCCTCAACATA 60
Db |||||
QY 61 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
Db |||||
QY 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
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QY 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
QY 181 GTGTTGCTTCTCATTCCATCTGGACCAAGGCTCCTGTGTCGAAGGCTCTTTGCGTGCA 240
Db |||||
QY 241 GAAGAGCTTTCCATCCAGGTGCATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAG 300
Db |||||
QY 301 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGT 360
Db |||||
QY 361 TTGCGCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420
Db |||||
QY 421 GGCTGGGTTGGAGATGGATTGATTCGTGGTCACTCTAGGATTAGCCCCAAACCCCAAGTGGG 480
Db |||||
QY 481 AAAAATGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
Db |||||
QY 541 TGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAATTCAGAAATTATCACCCACAAA 600
Db |||||
QY 601 GATCCCATATTTCAACACTCAAACCTGCAACACAAACACAGAAATTTATGTCAGTGACAGT 660
Db |||||
QY 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTCTACTACTCTCTCTGCT 720
Db |||||
QY 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTCTACTACTCTCTCTGCT 720

QY 721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTGCACAGAAAGTTTTATG 780
Db |||||
721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTGCACAGAAAGTTTTATG 780
QY 781 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTGAAAAATAAAGCAGCAATCAAG 840
Db |||||
781 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTGAAAAATAAAGCAGCAATCAAG 840
QY 841 AATGAAGCTGCTGGGTTTGGAGTGTCCCCACGGCTCTGCTAGTGTCTGCTCTCCTCTTC 900
Db |||||
841 AATGAAGCTGCTGGGTTTGGAGTGTCCCCACGGCTCTGCTAGTGTCTGCTCTCCTCTTC 900
QY 901 TTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCCCTTCCCT 960
Db |||||
901 TTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCCCTTCCCT 960
QY 961 TTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACCAAAAGTAGTAAAGGAGGAGAAG 1020
Db |||||
961 TTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACCAAAAGTAGTAAAGGAGGAGAAG 1020
QY 1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACTGATAAAAAACCCAGAGAGTCC 1080
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1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACTGATAAAAAACCCAGAGAGTCC 1080
QY 1081 AAGAGTCCAAGCAAAAACCTACCGTGGATGCCCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140
Db |||||
1081 AAGAGTCCAAGCAAAAACCTACCGTGGATGCCCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140
QY 1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCTGCCCGAGCTGGGAA 1200
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1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCTGCCCGAGCTGGGAA 1200
QY 1201 ATCAAAAGGCCAAAGAACCAAGAGAAAGTCCACCCCTTGGTTCCTAACTGGAATCAGC 1260
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QY 1261 TCAGGACTGCCATTGGACTATGGAGTGACCAAGAGAGATGCCCTTCTCCTTATTGTAAC 1320
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1261 TCAGGACTGCCATTGGACTATGGAGTGACCAAGAGAGATGCCCTTCTCCTTATTGTAAC 1320
QY 1321 CCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCACGGCTTTCTAGCCTGGCTAT 1380
Db |||||
1321 CCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCACGGCTTTCTAGCCTGGCTAT 1380
QY 1381 GTCTTAATAATATCCCACCTGGGAGAAAGGAGTTTGCAAAAGTGCAAGGACCTAAAAACATC 1440
Db |||||
1381 GTCTTAATAATATCCCACCTGGGAGAAAGGAGTTTGCAAAAGTGCAAGGACCTAAAAACATC 1440
QY 1441 TCATCAGTATCCAGTGGTAAAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1500
Db |||||
1441 TCATCAGTATCCAGTGGTAAAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1500
QY 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGAGCTCAGACCCCTTCTTCA 1560
Db |||||
1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGAGCTCAGACCCCTTCTTCA 1560
QY 1561 GCTCTGAAAGAGAAACA CGTATCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA 1620
Db |||||
1561 GCTCTGAAAGAGAAACACGATATCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA 1620
QY 1621 AGAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAAATCTGAGACCTAA 1680
Db |||||
1621 AGAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAAATCTGAGACCTAA 1680
QY 1681 TCTCTGTAAGCTAAAAATAAAGAAATPAGAAACAAAGGCTGAGGATACGACGTACACTGTCA 1740
Db |||||
1681 TCTCTGTAAGCTAAAAATAAAGAAATAGAAACAAGGCTGAGGATACGACGTACACTGTCA 1740
QY 1741 GCAGGACTGTAAACACAGACAGGGTCAAAAGTGTTTTCTCTGAACACATTTGAGTTGGAAT 1800
Db |||||
1741 GCAGGACTGTAAACACAGACAGGGTCAAAAGTGTTTTCTCTGAACACATTTGAGTTGGAAT 1800
QY 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACCTGCTGATATTTTCTCT 1860

Db |||||
1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860
QY 1861 AGGAAATATACTTTTACAGTAACAAAAATAAAAACTCTTATAAAATTTCTATTTTATCT 1920
Db |||||
1861 AGGAAATATACTTTTACAGTAACAAAAATAAAAACTCTATAAAATTTCTATTTTATCT 1920
QY 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
Db |||||
1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
QY 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGCAAGGTATTACACTC 2040
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QY 2041 TGTAATTGAATATTATTCCTCAAAAAAATGCACATAGTGAACGCTATCTGGGAAGCTAT 2100
Db |||||
2041 TGTAATTGAATATTATTCCTCAAAAAAATGCACATAGTGAACGCTATCTGGGAAGCTAT 2100
QY 2101 TTTTTCAGTTTGTATATTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTGTCTGA 2160
Db |||||
2101 TTTTTCAGTTTGTATATTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTGTCTGA 2160
QY 2161 GACTAATCTTATTCATTTTCTTAATATGGCAACCATTATAACCTTAATTTATTATTAAAC 2220
Db |||||
2161 GACTAATCTTATTCATTTTCTTAATATGGCAACCATTATAACCTTAATTTATTATTAAAC 2220
QY 2221 ATACCTAAGAAAGTACATTGTTACCTCTATATACCAAGCACATTTTAAAGTGCCATTAA 2280
Db |||||
2221 ATACCTAAGAAAGTACATTGTTACCTCTATATACCAAGCACATTTTAAAGTGCCATTAA 2280
QY 2281 CAAATGTATCAGTACGCCCCTCTTTTCCAAACAAGAGGAGCTGAGAGATGCAGAAATATT 2340
Db |||||
2281 CAAATGTATCAGTACGCCCCTCTTTTCCAAACAAGAGGAGCTGAGAGATGCAGAAATATT 2340
QY 2341 TGTGACAAAAAATTAAGCAATTTAGAAAAACTT 2372
Db |||||
2341 TGTGACAAAAAATTAAGCAATTTAGAAAAACTT 2372

Search completed: August 18, 2004, 19:19:42
Job time : 920 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 16, 2004, 12:05:52 ; Search time 6080 Seconds
(without alignments)
11650.180 Million cell updates/sec

Title: US-10-063-670-5
Perfect score: 2372
Sequence: 1 agcagggaatccggtgtc.....ttaaagcatttagaaaaatt 2372

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_htc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_htc:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: em_gss_hum:*
 - 18: em_gss_inv:*
 - 19: em_gss_pln:*
 - 20: em_gss_vrt:*
 - 21: em_gss_fun:*
 - 22: em_gss_mam:*
 - 23: em_gss_mus:*
 - 24: em_gss_pro:*
 - 25: em_gss_rod:*
 - 26: em_gss_phg:*
 - 27: em_gss_vrl:*
 - 28: gb_gss1:*
 - 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	1053.4	44.4	1143	9	AL574194
2	1043.8	44.0	1154	9	AL550279
3	1005.6	42.4	1201	9	AL541927
4	991.6	41.8	1201	9	AL550621

C 5	976.6	41.2	1201	13	BX397211	BX397211 BX397211
C 6	970.4	40.9	1201	9	AL547901	AL547901 AL547901
C 7	954.6	40.2	1073	9	AL552625	AL552625 AL552625
C 8	954.4	40.2	1201	9	AL546590	AL546590 AL546590
C 9	943.8	39.8	1015	9	AL552299	AL552299 AL552299
C 10	937.8	39.5	1157	9	AL575514	AL575514 AL575514
C 11	936	39.5	1201	13	BX366718	BX366718 BX366718
C 12	933	39.3	1007	9	AL575633	AL575633 AL575633
C 13	932.6	39.3	1201	9	AL574436	AL574436 AL574436
C 14	925.8	39.0	1201	9	AL546669	AL546669 AL546669
C 15	917.6	38.7	1201	9	AL541926	AL541926 AL541926
C 16	909.8	38.4	1201	9	AL547774	AL547774 AL547774
C 17	907.6	38.3	973	9	AL574433	AL574433 AL574433
C 18	902.2	38.0	1172	9	AL552127	AL552127 AL552127
C 19	899.8	37.9	978	9	AL573693	AL573693 AL573693
C 20	894	37.7	1201	9	AL544430	AL544430 AL544430
C 21	892.4	37.6	1116	9	AL552661	AL552661 AL552661
C 22	890.4	37.5	1201	13	BX402505	BX402505 BX402505
C 23	885.4	37.3	1201	9	AL571928	AL571928 AL571928
C 24	884.2	37.3	1201	9	AL546623	AL546623 AL546623
C 25	880	37.1	1200	9	AL574827	AL574827 AL574827
C 26	878.6	37.0	1172	9	AL550911	AL550911 AL550911
C 27	877.2	37.0	1201	9	AL551020	AL551020 AL551020
C 28	876.2	36.9	1067	9	AL552737	AL552737 AL552737
C 29	873.2	36.8	975	9	AL576740	AL576740 AL576740
C 30	872.8	36.8	1014	9	AL553858	AL553858 AL553858
C 31	870.4	36.7	1151	9	AL550829	AL550829 AL550829
C 32	868.6	36.6	1074	9	AL552777	AL552777 AL552777
C 33	865.4	36.5	1201	13	BX402504	BX402504 BX402504
C 34	861.4	36.3	957	9	AL576805	AL576805 AL576805
C 35	858	36.2	970	9	AL550615	AL550615 AL550615
C 36	854.4	36.0	1161	9	AL550876	AL550876 AL550876
C 37	852.2	35.9	919	9	AL570186	AL570186 AL570186
C 38	850.4	35.9	972	9	AL549512	AL549512 AL549512
C 39	848.4	35.8	1201	9	AL570563	AL570563 AL570563
C 40	838	35.3	911	9	AL543874	AL543874 AL543874
C 41	837	35.3	1201	13	BX334897	BX334897 BX334897
C 42	834.8	35.2	913	13	BX459046	BX459046 BX459046
C 43	831.2	35.0	1201	9	AL553712	AL553712 AL553712
C 44	826.8	34.9	1201	13	BX366589	BX366589 BX366589
C 45	821.2	34.6	863	9	AL571099	AL571099 AL571099

ALIGNMENTS

RESULT 1
AL574194/c
LOCUS AL574194 1143 bp mRNA linear EST 31-MAY-2003
DEFINITION AL574194 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI039YJ06 3-PRIME, mRNA sequence.
ACCESSION AL574194
VERSION AL574194.2 GI:31295529
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1143)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12934166.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI039DE03NP1&cluster=5952.r. Contact : Feng Liang Email : fliang@lifetech.com URL :

Db 64 CTCTCATATCACCAAGTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGAT 123

QY 162 GGCCAGGTGCTTCAGCCTGGTGTGTCTTCTCACTTGCATCTGGACCACGAGGCTCCTGGT 221

Db 124 GGCAGGTGCTTCAGCCTGGTGTGTCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGT 183

QY 222 CCAAGGCTCTTTGCGTGCAGAAAGCTTTCCATCCAGGTGTCTATGCAGAAATATAGGGGAT 281

Db 184 CCAAGGCTCTTTGCGTGCAGAAAGCTTTCCATCCAGGTGTCTATGCAGAAATATAGGGGAT 243

QY 282 CACCCTTGTGAGCAAAAAGCGGAACCAAGCAGCTGAATTTACAGAAGCTAAGAGGCCTG 341

Db 244 CACCCTTGTGAGCAAAAAGCGGAACCAAGCAGCTGAATTTACAGAAGCTAAGAGGCCTG 303

QY 342 TAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAG 401

Db 304 TAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAG 363

QY 402 CTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCACTCTAGGATTAG 461

Db 364 CTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCACTCTAGGATTAG 423

QY 462 CCCAAACCCCAAGTGTGGAAAAAATGGGGTGGGTCTCTGATTTTGGAGGTTCCAGTGAG 521

Db 424 CCCAAACCCCAAGTGTGGAAAAAATGGGGTGGGTCTCTGATTTTGGAGGTTCCAGTGAG 483

QY 522 CCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAATTCC 581

Db 484 CCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAATTCC 543

QY 582 AGAAATTATCACCAACAAAGATCCCATATTCAACACTCAAACTGCAACACAAACACAGA 641

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QY 642 ATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCC 701

Db 604 ATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCC 663

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Db 664 TACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATTG 723

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Db 964 AGTAGTAAAGGAGGAGGAGCCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACTGA 1023

QY 1062 TAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAAACCTACCGTGGATGCTGGAAGCTGA 1121

Db 1024 TAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAAACCTACCGTGGATGCTGGAAGCTGA 1083

QY 1122 AGTTTAGATGAGACAGAAATGAGGAGACACACTGAGGCTGGTTTCTTT 1170

Db 1084 AGTTTAGATGAGAGAAATRAG--AGAMACACTGAGGCTGGTTTCTTY 1130

LOCUS AL541927 1201 bp mRNA linear EST 12-MAY-2003

DEFINITION AL541927 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE007YF17 5-PRIME, mRNA sequence.

ACCESSION AL541927

VERSION AL541927.2 GI:30546572

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1201)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 15, 2001 this sequence version replaced gi:12873466.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5952.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DE007CC09QP1&cluster=5952.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ InvitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DE007CC09QP1.

FEATURES

Location/Qualifiers

1..1201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DE007YF17"

/tissue_type="PLACENTA"

/clone_lib="Homo sapiens PLACENTA"

/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 42.4%; Score 1005.6; DB 9; Length 1201;

Best Local Similarity 95.5%; Pred. No. 3.2e-202;

Matches 1060; Conservative 15; Mismatches 29; Indels 6; Gaps 4;

QY 1260 CTCAGGACTGCCATTGGACTATGGAGTGCACAAAGAGAATGCCCTTCTCCTATTGTAA 1319

Db 55 CCCGGGATTGCCATTGGACTATGGAGTGCACAAAGAGAATGCCCTTCTCCTATTGTAA 114

QY 1320 CCCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCACGGCCTTCTAGCCTGGCTA 1379

Db 115 CCCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCACGGCCTTCTAGCCTGGCTA 174

QY 1380 TGTCCCTAATAATATCCCACTGGGAGAAAGAGTTTGCAAAGTGCAGGACCTAAACAT 1439

Db 175 TGTCCCTAATAATATCCCACTGGGAGAAAGAGTTTGCAAAGTGCAGGACCTAAACAT 234

QY 1440 CTCATCAGTATCCAGTGGTAAAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAG 1499

Db 235 CTCATCAGTATCCAGTGGTAAAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAG 294

QY 1500 CCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGAGCTCAGACCCCTTCTTC 1559

Db 295 CCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGAGCTCAGACCCCTTCTTC 354

QY 1560 AGCTCTGAAAGAGAAAAACGATATCCCACTGCATGTCTTCTGAGCCCGGTAAGAGCAA 1619

Db 355 AGCTCTGAAAGAGAAAAACGATATCCCACTGCATGTCTTCTGAGCCCGGTAAGAGCAA 414

QY 1620 AAGAATGGCAGAAAAAGTTTAGCCCCCTGAAAGCCCATGGAGATTCTCATAACTTGAGACCTA 1679

Db 415 AAGAATGGCAGAAAAAGTTTAGCCCCCTGAAAGCCCATGGAGATTCTCATAACTTGAGACCTA 474

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QY 1680 ATCTCTGTAAGCTAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTC 1739
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Db 475 ATCTCTGTAAGCTAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTC 534

QY 1740 AGCAGGGACTGTAAACACAGACAGGGTCAAAAGTGTCTCTCTGTAACACATAGATTGGAA 1799
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Db 535 AGCAGGGACTGTAAACACAGACAGGGTCAAAAGTGTCTCTCTGTAACACATAGATTGGAA 594

QY 1800 TCACCTGTTTAGAACACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTC 1859
|||
Db 595 TCACCTGTTTAGAACACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTC 654

QY 1860 TAGGAAATATACCTTTTACAAGTAACAACAAATAAAAACTCTTATAAAATTTCTATTTTATC 1919
|||
Db 655 TAGGAAATATACCTTTTACAAGTAACAACAAATAAAAACTCTTATAAAATTTCTATTTTATC 714

QY 1920 TGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAA 1979
|||
Db 715 TGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAA 774

QY 1980 ATTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTCTGTGCAAGGTATTACACT 2039
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Db 775 ATTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTCTGTGCAAGGTATTACACT 834

QY 2040 CTGTAATTGAATATATTCTCTCAAAAAATTGCACATAGTAGAAAGCTATCTGGGAAGCTA 2099
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QY 2100 TTTTTCAGTTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTTTGCTG 2159
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Db 895 TTTTTCAGTTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTTTGCTG 954

QY 2160 AGACTAATCTTATTCATTTCTCTAATATGGCAACCAATTATAACCTTAATTTATTATTA 2219
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Db 955 AGACTAATCTTATTCATTTCTCTAATATGGSAACCAATTATAACCTTAATTTATTATTA 1014

QY 2220 CATACCTAAGAAGTACATTTGTACCTCTATATACCAAGCACATTTTAAAAAGTGCCATTA 2279
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Db 1015 CATACCTAAG-AGKACATGTTTACCTCTATATACCAAGMCM--TTTAAAAAGTGCMTTA 1071

QY 2280 ACAAATGTATCAGCCCTCCTTTTCCAAACAAGAGGCACTGAGAGATGCAGAAATAT 2339
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QY 2340 TTGTGACAAAAAATTAAAGCATTTAGAAAA 2369
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Db 1129 GTRMAAAATWAASMTWGAACCTAAAAA 1158
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RESULT 4
AL550621 1201 bp mRNA linear EST 31-MAY-2003
LOCUS AL550621 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
DEFINITION clone CS0DI058YN14 5-PRIME, mRNA sequence.
ACCESSION AL550621
VERSION AL550621.2 GI:31272438
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12887768.
Contact: Genoscope
Genoscope - Centre National de Sequenage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
```

more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI058DG07QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI058DG07QP1.
Location/Qualifiers
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI058YN14"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source

ORIGIN

Query Match 41.8%; Score 991.6; DB 9; Length 1201;
Best Local Similarity 98.5%; Pred. No. 2.9e-199;
Matches 989; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 67 GAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCACTGGCCATCTG 126
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Db 65 GAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCACTGGCCATCTG 124
|||
QY 127 AGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTCTTTCAGCCTGGTGTG 186
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Db 125 AGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTCTTTCAGCCTGGTGTG 184
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QY 187 CTTCTCATTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTCGTCGAGAAAGAG 246
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Db 185 CTTCTCATTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTCGTCGAGAAAGAG 244
|||
QY 247 CTTTCCATCCAGGTGTCATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAGCGAAC 306
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Db 245 CTTTCCATCCAGGTGTCATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAGCGAAC 304
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QY 307 CAGCAGCTGAATTCACAGAAAGCTAAGGAGCGCTGTAGGCTGTGGGACTAAGTTTGGCC 366
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Db 305 CAGCAGCTGAATTCACAGAAAGCTAAGGAGCGCTGTAGGCTGTGGGACTAAGTTTGGCC 364
|||
QY 367 GGCAAGGACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTATGGCTGG 426
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Db 365 GGCAAGGACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTATGGCTGG 424
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QY 427 GTTGGAGATGGATTCGTGGTCACTCTCTAGGATTAGCCCAACCCCAAGTGGGAAAAAAT 486
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Db 425 GTTGGAGATGGATTCGTGGTCACTCTCTAGGATTAGCCCAACCCCAAGTGGGAAAAAAT 484
|||
QY 487 GGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTAC 546
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Db 485 GGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTAC 544
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QY 547 AACTCATCTGATCTTGGACTAACTCGTGCATTCCAGAAATTATCACCCACCAAGATCCC 606
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QY 607 ATATTCAACACTCAAACCTGCAACACAAACAGAAATTTATTGTCAGTGACAGTACCTAC 666
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Db 605 ATATTCAACACTCAAACCTGCAACACAAACAGAAATTTATTGTCAGTGACAGTACCTAC 664
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QY 667 TCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTACTCCTCCTGCCAGCT 726
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Db 665 TCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTACTCCTCCTGCCAGCT 724
|||
QY 727 TCCACTTCTATTCACGGAGAAAAAATTTGATTGTGTACAGAAAGTTTTTATGGAAGT 786
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Db 725 TCCACTTCTATTCACGGAGAAAAAATTTGATTGTGTACAGAAAGTTTTTATGGAAGT 784
|||
QY 787 AGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAGAAATGAA 846
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Db	785		AGCACCATG	CTC	CAGAAA	CTGA	ACCATT	TGTTG	TGAAAA	TAAAG	CAGCAT	TTCA	GAA	844	
QY	847		GCTGCTGGG	TTT	GAGAGT	GTCCC	CACGG	CTCTG	CTAGT	CTTG	CTCTCT	CTTT	TGGT	906	
Db	845		GCTGCTGGG	TTT	GAGAGT	GTCCC	CACGG	CTCTG	CTAGT	CTTG	CTCTCT	CTTT	TGGT	904	
QY	907		GCTGCAG	CTGGT	CTTGG	ATTTT	TGCTAT	GTCAA	AAAGT	TATGT	GAAGG	CCCTT	CCCTTTT	TACA	966
Db	905		GCTGCAG	CTGGT	CTTGG	ATTTT	TGCTAT	GTCAA	AAAGT	TATGT	GAAGG	CCCTT	CCCTTTT	TACA	964
QY	967		AACAAGA	AAT	CAGCAGA	AGGAA	ATGAT	CGAAA	CCAA	AGTAG	TAAAG	GAGG	AGAGG	CCCAAT	1026
Db	965		AAMAARA	AAT	CAGCMGA	AGGAA	ATGWT	CGAD	ACCM	AACTAG	TAAAG	GAGG	AGAGG	CCCAAT	1024
QY	1027		GATAGCA	ACCC	TATGAG	GGAAT	CAAA	GAAAA	CTGAT	TAAAA	CCCC				1070
Db	1025		GATWAS	CACCC	YAATGAG	GGAT	CAA	GAAAA	CTGWT	AAAA	CCCC				1068

RESULT 5	
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LOCUS	BX397211
DEFINITION	1201 bp mRNA linear EST 13-MAY-2003 BX397211 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI031YH11 3-PRIME, mRNA sequence.

ORIGIN

	Query Match	41.2%;	Score 976.6;	DB 13;	Length 1201;
	Best Local Similarity	97.5%;	Pred. No. 4.4e-196;		
	Matches 982;	Conservative 16;	Mismatches 8;	Indels 1;	Gaps 1;
QY	1332	CCTATCCTCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCCCTGGCTATGTCCTAATAAT	1391		
		: : : : :			
Dd	1006	YCYACCCCCCTACCTCCAATGTCTCCCACTGCCTTCTWK -CTTKCTWTKTCTAATAAT	948		
QY	1392	ATCCCACTGGGAGAAAGGAGTTTTTGCAAAGTGC AAGGACCCTAAAACATCTCATCAGTATC	1451		
		: : : : : : :			
Dd	947	AYCCCACTGKGAGAAAGGAKT TTTKCAAAKTGCAWKKACCTAAAAACATCTCATCAGTATC	888		

QY	1452	CAGTGGTAAAAAGGCCTCCTGGCTGTCCTGAGCTAGGTGGTGTGAAAGCCAAAGGAGTCAC	1511
Db	887	CAGTGGTAAAAAGGCCTCCTGGCTGTCCTGAGCTAGGTGGTGTGAAAGCCAAAGGAGTCAC	828
QY	1512	TGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTTCAGCTCTGAAAGA	1571
Db	827	TGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTTCAGCTCTGAAAGA	768
QY	1572	GAAACACGTATCCACCTGACATGTCCTTCTGAGCCCGGTAAAGAGCAAAAGAAATGGCAGA	1631
Db	767	GAAACACGTATCCACCTGACATGTCCTTCTGAGCCCGGTAAAGAGCAAAAGAAATGGCAGA	708
QY	1632	AAAGTTTAGCCCTGAAAAGCCATGGAGATTCTCATAACTTGAGACCTTAATCTCTGTAAAG	1691
Db	707	AAAGTTTAGCCCTGAAAAGCCATGGAGATTCTCATAACTTGAGACCTTAATCTCTGTAAAG	648
QY	1692	CTAAATTAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTGAGCAGGACTGT	1751
Db	647	CTAAATTAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTGAGCAGGACTGT	588
QY	1752	AAACACAGACAGGGTCAAAGTGTCTTCTGAAACACATTGAGTTGGAATCACTGTTTAGA	1811
Db	587	AAACACAGACAGGGTCAAAGTGTCTTCTGAAACACATTGAGTTGGAATCACTGTTTAGC	528
QY	1812	ACACACACACTTACTTTTCTGGTCTCTACCACCTGCTGATATTTTCTGAGGAAATATAC	1871
Db	527	ACACACACACTTACTTTTCTGGTCTCTACCACCTGCTGATATTTTCTGAGGAAATATAC	468
QY	1872	TTTTACAAGTAACAAAACTCTTATAAATTTCTATTTTTTATCTGAGTTACAGAA	1931
Db	467	TTTTACAAGTAACAAAACTCTTATAAATTTCTATTTTTTATCTGAGTTACAGAA	408
QY	1932	ATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCACACAAACA	1991
Db	407	ATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCACACAAACA	348
QY	1992	TTTGCTGAATAGCTACTATATGTCAGTGCTGTGCAAGGTATTACACTCTGTAATTGAAT	2051
Db	347	TTTGCTGAATAGCTACTATATGTCAGTGCTGTGCAAGGTATTACACTCTGTAATTGAAT	288
QY	2052	ATTATTCTCAAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTCAGTT	2111
Db	287	ATTATTCTCAAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTCAGTT	228
QY	2112	TTGATATTTCTAGCTTATCTACTTCCAAAACCTAATTTTTTATTTTTGCTGAGACTAATCTTA	2171
Db	227	TTGATATTTCTAGCTTATCTACTTCCAAAACCTAATTTTTTATTTTTGCTGAGACTAATCTTA	168
QY	2172	TTCAATTTTCTCTAATATGGCAACCATTAACCTTAATTTATTATTAAACATACCTAAGAA	2231
Db	167	TTCAATTTTCTCTAATATGGCAACCATTAACCTTAATTTATTATTAAACATACCTAAGAA	108
QY	2232	GTACATTGTTACCTCTATATACCAAGCACATTTTAAAGTGCCATTAAACAAATGTATCA	2291
Db	107	GTACATTGTTACCTCTATATACCAAGCACATTTTAAAGTGCCATTAAACAAATGTATCA	48
QY	2292	CTAGCCCTCCTTTTTTCCAAACAAGGAGCTGAGAGATGCAGAAATA	2338
Db	47	CTAGCCCTCCTTTTTTCCCAACAAGAGGAGCTGAGAGATGCAGAAATA	1

RESULT 6	
AL547901/c	
LOCUS	AL547901 1201 bp mRNA linear EST 31-MAY-2003
DEFINITION	AL547901 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI033YD11 3-PRIME, mRNA sequence.
ACCESSION	AL547901
VERSION	AL547901.2 GI:31269729
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:

REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12882399.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI033CB06NP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI033CB06NP1.
FEATURES
source Location/Qualifiers
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
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/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 40.9%; Score 970.4; DB 9; Length 1201;
Best Local Similarity 98.6%; Pred. No. 9e-195;
Matches 986; Conservative 7; Mismatches 5; Indels 2; Gaps 2;
QY 1338 CTCCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCGTGGCTATGTCCTAATAATATCCCA 1397
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QY 1398 CTGGGAGAAAGGAGTTTGCAAAGTGCAAGGACCTTAAACATCTCATCAGTATCCAGTGG 1457
Db 958 CTGGGAGAAAGGAGTTTGCAAAGTGCAAGGACCTTAAACATCTCATCAGTATCCAGTGG 899
QY 1458 TAAAAGGCCCTCCTGGTGTCTGAGGCTAGGTGGTTGAAAGCCCAAGGAGTCACTGAGAC 1517
Db 898 TAAAAGGCCCTCCTGGTGTCTGAGGCTAGGTGGTTGAAAGCCCAAGGAGTCACTGAGAC 839
QY 1518 CAAGGCTTTTCTACTGATTCCGCAGCTCAGACCCCTTCTTCAGCTCTGAAAGAGAAACA 1577
Db 838 CAAGGCTTTTCTACTGATTCCGCAGCTCAGACCCCTTCTTCAGCTCTGAAAGAGAAACA 779
QY 1578 CGTATCCCACCTGACATGTCCTTCTGAGCCCGGTAAAGCAAAAGAAATGGCAGAAAAGTT 1637
Db 778 CGTATCCCACCTGACATGTCCTTCTGAGCCCGGTAAAGCAAAAGAAATGGCAGAAAAGTT 719
QY 1638 TAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAGCTTAAAA 1697
Db 718 TAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAARGTAAAA 659
QY 1698 TAAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACTGTCCAGCGGACTGTAAACAC 1757
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Db 598 AGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAATCACTGTTTRGAACACAC 539
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Db 538 ACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTTAGGAAATATACITTTAC 479
QY 1878 AAGTAACAAAATAAAAACTCTTATAAAATTTCTATTTTATCTGAGTTACAGAAATGATT 1937

Db 478 AAGTAACAAAATAAAAACTCTTATAAAATTTCTATTTTATCTGAGTTACAGAAATGATT 419
QY 1938 ACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCACAAACATTTGCT 1997
Db 418 ACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCACAAACATTTGCT 359
QY 1998 GAATAGCTACTATATGTCAAAGTGTCTGCGAAGGTATTACACTCTGTAATTGAATATT 2057
Db 358 GAATAGCTACTATATGTCAAAGTGTCTGCGAAGGTATTACACTCTGTAATTGAATATT 299
QY 2058 CCTCAAAAATTGCACATAGTAGAACGCTATCTCTGGGAAGCTATTTTTTTCAGTTTTGATA 2117
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QY 2118 TTTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTGTCTGAGACTAATCTTATTCTATT 2177
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Db 178 TTCTCTAATATGSCAACCATTTATAACCTTTAATTTATTATTATTNACATACCTTAAGAAGTACAT 119
QY 2238 TGTTCCTCTATATACCAAAGCACATTTTAAAGTGCCATTAAACAAATGTATCACTAGGCC 2297
Db 118 TGTTCCTCTATATACCAAAGCACATTTTAAAGTGCCATTAAACAAATGTATCACTAGGCC 59
QY 2298 CTCCTTTTCCAAAGAAGGGACTGAGAGATGCGAGAAAT 2337
Db 58 CTCCTTTTCCAAAGANGGGACTGAGAGATGCGAGAAAT 19

RESULT 7
AL552625/c
LOCUS AL552625 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI067YG15 3-PRIME, mRNA sequence.
ACCESSION AL552625
VERSION AL552625.2 GI:31274440
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1073)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12891706.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI067AD08NP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI067AD08NP1.
FEATURES
source Location/Qualifiers
1..1073
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI067YG15"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."


```
QY 1164 TTTCTTTTCATGCTCCTTACCTGCCCCAGCTGGGAAATCAAAAGGGCCAAAGAACCAAA 1223
Db 729 TTTCTTTTCATGCTCCTTACCTGCCCCAGCTGGGAAATCAAAAGGGCCAAAGAACCAAA 670

QY 1224 GAAGAAAGTCCACCCCTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGG 1283
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QY 1284 AGTGCACCAAGAGAAATGCCCTTCTCCTTTATTGTAACCCCTGTCTGGATCCTATCCTCTA 1343
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QY 1464 GGCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGCCAAAGGAGTCACTGAGACCAAGGC 1523
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QY 1524 TTTCTCTACTGATTCGCGAGCTCAGACCCCTTTCTTTCAGCTCTGAAAGAGAAACACGTATC 1583
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QY 1764 GGTCAAAGTGTTTTCTCTGAACACATTTGAGTTGGAAATCACTGTTTAGAACACACACACTT 1823
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QY 1824 ACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCTAGGAAATATACTTTTACAAGTAA 1883
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QY 1884 CAAAAATAA 1892
Db 9 NNWNWGAW 1
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LOCUS AL552299 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI069YN02 5-PRIME, mRNA sequence.
ACCESSION AL552299
VERSION AL552299.2 GI:31274114
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1015)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL On Feb 15, 2001 this sequence version replaced gi:12891068.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
```

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI069DG01QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI069DG01QP1.

FEATURES

source
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/clone="CS0DI069YN02"
/tissue_type="PLACENTA COT 25-NORMALIZED"
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/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 39.8%; Score 943.8; DB 9; Length 1015;
Best Local Similarity 99.8%; Pred. No. 3.9e-189;
Matches 945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 78 CCGGACTAGTTATTGAGCATCTGCCCTCTCATATACCCAGTGGCCATCTGAGGTGTTTCCC 137
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QY 438 ATTCTGTGTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAAATGGGTGGGTGT 497
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QY 498 CCTGATTGTGGAAGGTTCCAGTGAGCCGACAGTTTGACGCTATTGTTACAACATCACTGA 557
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QY 678 CCCTTACTCTACAATACCTGCCCCCTACTACTCTCTCTGCTCCAGCTTCCACTTCTAT 737
Db 662 CCCTTACTCTACAATACCTGCCCCCTACTACTCTCTCTGCTCCAGCTTCCACTTCTAT 721
QY 738 TCCACGGAGAAAAAATTGATTGTGTCACAGAAAGTTTTATGGAAACTAGCACCATGTC 797

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0AI040CB02QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0AI040CB02QP1.

FEATURES
source

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/tissue_type="PLACENTA COT 25-NORMALIZED"
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/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 39.5%; Score 936; DB 13; Length 1201;
Best Local Similarity 97.6%; Pred. No. 1.7e-187;
Matches 953; Conservative 15; Mismatches 6; Indels 2; Gaps 2;

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QY 72 CTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGTG 131
Db 124 CTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGTG 183

QY 132 TTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGTGCTTCAGCCTGGTGTGCTTCT 191
Db 184 TTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGTGCTTCAGCCTGGTGTGCTTCT 243

QY 192 CACTTCCATCTGGACCAACGAGGCTCCTGGTCCAGGCTTTGCGTGCAGAGAGTTTC 251
Db 244 CACTTCCATCTGGACCAACGAGGCTCCTGGTCCAGGCTTTGCGTGCAGAGAGTTTC 303

QY 252 CATCCAGGTGTCATGCAGAAATTATGGGGATCACCCCTTGAGCAAAAAGCGGAACAGCA 311
Db 304 CATCCAGGTGTCATGCAGAAATTATGGGGATCACCCCTTGAGCAAAAAGCGGAACAGCA 363

QY 312 GCTGAATTTACAGAGCTAAGGAGGCGCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAA 371
Db 364 GCTGAATTTACAGAGCTAAGGAGGCGCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAA 423

QY 372 GGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAACTTCAGCTATGGCTGGGTGG 431
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QY 552 ATCTGACTTGGACTAACTCGTGCAATTCAGAAATTATCACCACCAAGATCCCATATT 611

Db 604 ATCTGATACTTGGACTAACTCGTGCAATTCAGAAATTATCACCACCAAGATCCCATATT 663

QY 612 CAACACTCAAACTGCAACACAACAACAAGAAATTTATTGTGAGTGACAGTACCTACTCGGT 671
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QY 672 GGCATCCCCTTACTCTACAATACCTGCCCTACTACTACTCTCCTCCTGCTCCAGCTTCCAC 731
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QY 972 GAATCAGCAGAGAGAA 987
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RESULT 12
AL575633/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AL575633 1007 bp mRNA linear EST 01-JUN-2003
AL575633 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI069YN02 3-PRIME, mRNA sequence.
AL575633
AL575633.2 GI:31313940
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1007)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12936986.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI069DG01NP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
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Location/Qualifiers
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source

1. 1007
/organism="Homo sapiens"
/mol_type="mRNA"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match		39.3%;	Score 933;	DB 9;	Length 1007;				
Best Local Similarity		96.4%;	Pred. No. 7.5e-187;						
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QY	889	GCTCTCCTCTCTTTGGTGGCTGCAGCTGGTCTTTGGATTGTTGCTATGTCAAAAGGATGTTG	948						
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QY	1009	AAGGAGGAGAAAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACTGATAAAAAAC	1068						
Db	890	AAGGAGGAGAAAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACTGATAAAAAAC	831						
QY	1069	CCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAGCTGAAGTTTAG	1128						
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QY	1129	ATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCGCTGCC	1188						
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Db	170	CAGTACACTGTGAGGGGACTGTAAACACAGACAGGGTCAAAGTGTCTTCTCTGAACAC	111						
QY	1788	ATTGAGTTGGAATCACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTA-CCACTG	1846						
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DEFINITION		AL574436 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI058YN14 3-PRIME, mRNA sequence.							
ACCESSION		AL574436							
VERSION		AL574436.2	GI:31312754						
KEYWORDS		EST.							
SOURCE		Homo sapiens (human)							
ORGANISM		Homo sapiens							
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.							
AUTHORS		1 (bases 1 to 1201)							
TITLE		Li,W.B., Gruber,C., Jessee,J. and Polayes,D.							
JOURNAL		Full-length cDNA libraries and normalization							
COMMENT		Unpublished (2001)							
		On Feb 16, 2001 this sequence version replaced gi:12934641.							
		Contact: Genoscope							
		Genoscope - Centre National de Sequencage							
		BP 191 91006 EVRY cedex - France							
		Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr							
		Library was constructed by Life Technologies, a division of							
		Invitrogen. This sequence belongs to sequence cluster 5952.r For							
		more information about this cluster, see							
		http://www.genoscope.cns.fr/							
		cgi-bin/cluster.cgi?seq=CS0DI058DG07NP1&cluster=5952.r. Contact :							
		Feng Liang Email : fliang@lifetech.com URL :							
		http://fulllength.invitrogen.com/ InvitroGen Corporation 1600							
		Faraday Avenue Genoscope sequence ID : CS0DI058DG07NP1.							
FEATURES		Location/Qualifiers							
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		digested with Not I and cloned into the Not I and EcoR V							
		sites of the pCMVSPORT 6 vector. Library was normalized."							
ORIGIN									
Query Match		39.3%;	Score 932.6;	DB 9;	Length 1201;				
Best Local Similarity		95.7%;	Pred. No. 9e-187;						
Matches 979;		Conservative 16;	Mismatches 23;	Indels 5;	Gaps 4;				
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QY	1397	ACTGGGAGAAAGGAGTTTGCAAAGTGCAAGGACCTAAACATCTCATCAGTATCCAGTG	1456						
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QY	1637	TTAGCCCTGAAAGCCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAAGCTAAA	1696						
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Db      486 CAAGTAACAAAAATAAAAACTCTTATAAAATTTCTATTTTATCTGAGTTACAGAAAATGAT 427
QY      1937 TACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCAACAAACATTTGC 1996
Db      426 TACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCAACAAACATTTGC 367
QY      1997 TGAATAGCTACTATATGTCAAGTCTGTGCAAGGTATTACACTCTGTGTAATTGAATATTAT 2056
Db      366 TGAATAGCTACTATATGTCAAGTCTGTGCAAGGTATTACACTCTGTGTAATTGAATATTAT 307
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QY      2354 TAA 2356
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AL546669
LOCUS
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AL546669 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI029YJ09 5-PRIME, mRNA sequence.
ACCESSION
AL546669
VERSION
AL546669.2 GI:31268502
KEYWORDS
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ORGANISM
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12880008.
Contact: Genoscope
Genoscope - Centre National de Sequenage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
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Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
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digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 39.0%; Score 925.8; DB 9; Length 1201;
Best Local Similarity 95.3%; Pred. No. 2.5e-185;
Matches 983; Conservative 4; Mismatches 36; Indels 8; Gaps 3;

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3-PRIME, mRNA sequence.
ACCESSION AL541926
VERSION AL541926.2 GI:30546570
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12873464.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE007CC09NPl&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
ORIGIN
Query Match 38.7%; Score 917.6; DB 9; Length 1201;
Best Local Similarity 90.5%; Pred. No. 1.3e-183;
Matches 984; Conservative 39; Mismatches 56; Indels 8; Gaps 5;
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Job time : 6086 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 16, 2004, 22:49:08 ; Search time 1034 Seconds
(without alignments)

11255.777 Million cell updates/sec

Title: US-10-063-670-5

Perfect score: 2372

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 800 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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82	2372	100.0	2372	13	US-10-063-553-5 Sequence 5, Appli
83	2372	100.0	2372	13	US-10-063-554-5 Sequence 200, App
84	2372	100.0	2372	13	US-10-298-993-200 Sequence 31, Appl
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238	2372	100.0	2404	9	US-09-833-381-849	Sequence 849, App	c 311	53	2.2	13574	15	US-10-311-455-1290	Sequence 1290, Ap
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240	2342.2	98.7	2369	16	US-10-264-237-1260	Sequence 1260, Ap	313	52.6	2.2	843	16	US-10-027-632-7034	Sequence 7034, Ap
241	2313.2	97.5	2324	13	US-10-276-774-999	Sequence 999, App	c 314	52.4	2.2	3252	13	US-10-027-632-113786	Sequence 113786,
242	2290.2	96.6	2313	15	US-10-291-634-1	Sequence 1, Appli	c 315	52.4	2.2	3252	13	US-10-027-632-113787	Sequence 113787,
243	1994	84.1	2029	15	US-10-079-111-2	Sequence 2, Appli	c 316	52.4	2.2	3252	13	US-10-027-632-113788	Sequence 113788,
244	967.4	40.8	1127	16	US-10-138-588-1	Sequence 1, Appli	c 317	52.4	2.2	3252	16	US-10-027-632-113786	Sequence 113786,
245	603.6	25.4	1896	10	US-09-866-050A-595	Sequence 595, App	c 318	52.4	2.2	3252	16	US-10-027-632-113787	Sequence 113787,
246	603.6	25.4	1896	15	US-10-152-661-595	Sequence 595, App	c 319	52.4	2.2	3252	16	US-10-027-632-113788	Sequence 113788,
c 247	500.2	21.1	516	9	US-09-962-436-348	Sequence 348, App	c 320	51.8	2.2	755	13	US-10-027-632-128109	Sequence 128109,
c 248	500.2	21.1	516	9	US-09-954-456-834	Sequence 834, App	c 321	51.8	2.2	755	16	US-10-027-632-128109	Sequence 128109,
c 249	500.2	21.1	516	9	US-09-954-456-1259	Sequence 1259, Ap	c 322	51.8	2.2	9832	15	US-10-311-455-629	Sequence 629, App
c 250	500.2	21.1	516	9	US-09-880-107-114	Sequence 114, App	c 323	51.6	2.2	16750	13	US-10-221-714A-36	Sequence 36, Appl
c 251	500.2	21.1	516	9	US-09-954-531-633	Sequence 633, App	c 324	51.6	2.2	16750	15	US-10-311-455-494	Sequence 494, App
c 252	500.2	21.1	516	9	US-09-954-531-1042	Sequence 1042, Ap	c 325	51.4	2.2	3673778	15	US-10-312-841-2	Sequence 2, Appli
c 253	485.8	20.5	506	9	US-09-778-320-96	Sequence 96, Appl	326	51	2.2	20579	17	US-10-433-793-104	Sequence 104, App
254	485.8	20.5	506	9	US-09-910-689-96	Sequence 96, Appl	c 327	50.8	2.1	5407	15	US-10-311-455-2063	Sequence 2063, Ap
255	485.8	20.5	506	14	US-10-010-742-96	Sequence 96, Appl	c 328	50.6	2.1	392	9	US-09-960-352-4808	Sequence 4808, Ap
256	485.8	20.5	506	17	US-10-714-389-96	Sequence 96, Appl	c 329	50.6	2.1	5504	13	US-10-221-613-270	Sequence 270, App
257	485.8	20.5	506	17	US-10-717-296-96	Sequence 96, Appl	c 330	50.4	2.1	12237	15	US-10-311-455-2331	Sequence 2331, Ap
258	440	18.5	486	10	US-09-918-995-10116	Sequence 10116, A	331	50	2.1	50	9	US-09-909-320-205	Sequence 205, App
259	419.4	17.7	472	10	US-09-918-995-9451	Sequence 9451, Ap	332	50	2.1	50	9	US-09-909-088B-205	Sequence 205, App
260	406	17.1	499	10	US-09-918-995-17297	Sequence 17297, A	333	50	2.1	50	9	US-09-905-291A-205	Sequence 205, App
261	403	17.0	441	10	US-09-918-995-4294	Sequence 4294, Ap	334	50	2.1	50	9	US-09-902-853-205	Sequence 205, App
262	397	16.7	411	10	US-09-918-995-8107	Sequence 8107, Ap	335	50	2.1	50	9	US-09-907-824-205	Sequence 205, App
c 263	387.6	16.3	820	15	US-10-079-111-5	Sequence 5, Appli	336	50	2.1	50	9	US-09-907-824-205	Sequence 205, App
c 264	334	14.1	339	15	US-10-291-634-11	Sequence 11, Appl	337	50	2.1	50	10	US-09-904-011-205	Sequence 205, App
265	328.6	13.9	559	15	US-10-079-111-3	Sequence 3, Appli	338	50	2.1	50	10	US-09-906-742-205	Sequence 205, App
266	318.4	13.4	334	13	US-10-085-783A-42439	Sequence 42439, A	339	50	2.1	50	10	US-09-906-838-205	Sequence 205, App
267	318.4	13.4	334	16	US-10-242-535A-42439	Sequence 42439, A	340	50	2.1	50	10	US-09-907-613-205	Sequence 205, App
268	296.8	12.5	492	15	US-10-291-634-12	Sequence 12, Appl	341	50	2.1	50	10	US-09-907-942-205	Sequence 205, App
c 269	239	10.1	241	9	US-09-604-287A-324	Sequence 324, App	342	50	2.1	50	10	US-09-904-859-205	Sequence 205, App
c 270	239	10.1	241	10	US-09-551-621-324	Sequence 324, App	343	50	2.1	50	10	US-09-909-204-205	Sequence 205, App
c 271	239	10.1	241	14	US-10-007-805-324	Sequence 324, App	344	50	2.1	50	10	US-09-904-820-205	Sequence 205, App
c 272	239	10.1	241	15	US-10-076-622-324	Sequence 324, App	345	50	2.1	50	10	US-09-904-786-205	Sequence 205, App
c 273	239	10.1	241	15	US-10-124-805-324	Sequence 324, App	346	50	2.1	50	10	US-09-906-646-205	Sequence 205, App
c 274	238	10.0	308	9	US-09-880-107-1687	Sequence 1687, Ap	347	50	2.1	50	10	US-09-906-700-205	Sequence 205, App
c 275	238	10.0	308	9	US-09-954-531-654	Sequence 654, App	348	50	2.1	50	10	US-09-903-786-205	Sequence 205, App
c 276	238	10.0	308	9	US-09-954-531-1067	Sequence 1067, Ap	349	50	2.1	50	10	US-09-902-903-205	Sequence 205, App
c 277	238	10.0	308	9	US-09-954-531-1068	Sequence 1068, Ap	350	50	2.1	50	10	US-09-903-749A-205	Sequence 205, App
c 278	237	10.0	241	9	US-09-604-287A-323	Sequence 323, App	351	50	2.1	50	10	US-09-904-119-205	Sequence 205, App
c 279	237	10.0	241	10	US-09-551-621-323	Sequence 323, App	352	50	2.1	50	10	US-09-902-936-205	Sequence 205, App
c 280	237	10.0	241	14	US-10-007-805-323	Sequence 323, App	353	50	2.1	50	10	US-09-907-794-205	Sequence 205, App
c 281	237	10.0	241	15	US-10-076-622-323	Sequence 323, App	354	50	2.1	50	10	US-09-903-943-205	Sequence 205, App
c 282	237	10.0	241	15	US-10-124-805-323	Sequence 323, App	355	50	2.1	50	10	US-09-904-462-205	Sequence 205, App
c 283	226.2	9.5	239	9	US-09-954-456-913	Sequence 913, App	356	50	2.1	50	10	US-09-902-736-205	Sequence 205, App
c 284	226.2	9.5	239	9	US-09-954-456-1513	Sequence 1513, Ap	357	50	2.1	50	10	US-09-907-925-205	Sequence 205, App
c 285	226.2	9.5	239	9	US-09-880-107-725	Sequence 725, App	358	50	2.1	50	10	US-09-902-692-205	Sequence 205, App
c 286	226.2	9.5	239	9	US-09-954-531-875	Sequence 875, App	359	50	2.1	50	10	US-09-903-520-205	Sequence 205, App
c 287	226.2	9.5	239	9	US-09-954-531-1285	Sequence 1285, Ap	360	50	2.1	50	10	US-09-905-056-205	Sequence 205, App
c 288	226.2	9.5	239	15	US-10-291-634-14	Sequence 14, Appl	361	50	2.1	50	10	US-09-909-064-205	Sequence 205, App
c 289	212.2	8.9	279	15	US-10-079-111-4	Sequence 4, Appli	362	50	2.1	50	10	US-09-904-553-205	Sequence 205, App
290	191.4	8.1	466	15	US-10-291-634-13	Sequence 13, Appl	363	50	2.1	50	10	US-09-905-381-205	Sequence 205, App
291	179.2	7.6	469	9	US-09-864-761-2325	Sequence 2325, Ap	364	50	2.1	50	10	US-09-905-088-205	Sequence 205, App
292	175	7.4	457	9	US-09-864-761-15431	Sequence 15431, A	365	50	2.1	50	10	US-09-907-575-205	Sequence 205, App
293	160	6.7	498	15	US-10-291-634-15	Sequence 15, Appl	366	50	2.1	50	10	US-09-902-759-205	Sequence 205, App
294	129	5.4	141	9	US-09-864-761-19060	Sequence 19060, A	367	50	2.1	50	10	US-09-902-759-205	Sequence 205, App
295	106	4.5	106	9	US-09-864-761-31946	Sequence 31946, A	368	50	2.1	50	10	US-09-902-634-205	Sequence 205, App
c 296	96.8	4.1	467	16	US-10-191-803-1134	Sequence 1134, Ap	369	50	2.1	50	10	US-09-902-713-205	Sequence 205, App
c 297	93	3.9	836	13	US-10-027-632-148987	Sequence 148987,	370	50	2.1	50	10	US-09-907-979-205	Sequence 205, App
c 298	60	2.5	60	10	US-09-908-975-10869	Sequence 10869, A	371	50	2.1	50	10	US-09-902-615-205	Sequence 205, App
c 299	58.2	2.5	641	12	US-09-969-034-389	Sequence 389, App	372	50	2.1	50	10	US-09-903-925-205	Sequence 205, App
c 300	58	2.4	3673778	15	US-10-312-841-2	Sequence 2, Appli	373	50	2.1	50	10	US-09-906-760A-205	Sequence 205, App
301	56.6	2.4	6216	17	US-10-257-166-13	Sequence 13, Appl	374	50	2.1	50	10	US-09-903-823-205	Sequence 205, App
c 302	55	2.3	83391	17	US-10-433-793-123	Sequence 123, App	375	50	2.1	50	10	US-09-907-652-205	Sequence 205, App
c 303	54.2	2.3	15373	15	US-10-311-455-440	Sequence 440, App	376	50	2.1	50	10	US-09-902-572A-205	Sequence 205, App
c 304	53.8	2.3	11790	15	US-10-311-455-515	Sequence 515, App	377	50	2.1	50	10	US-09-902-979-205	Sequence 205, App
c 305	53.4	2.3	3673778	15	US-10-312-841-1	Sequence 1, Appli	378	50	2.1	50	10	US-09-905-125-205	Sequence 205, App
c 306							379	50	2.1	50	10	US-09-906-815A-205	Sequence 205, App

380	50	2.1	50	10	US-09-905-449-205	Sequence 205, App	453	48.2	2.0	3476	13	US-10-245-752-51	Sequence 51, Appl
381	50	2.1	50	10	US-09-903-806-205	Sequence 205, App	454	48.2	2.0	3476	13	US-10-245-859-51	Sequence 51, Appl
382	50	2.1	50	10	US-09-904-992-205	Sequence 205, App	455	48.2	2.0	3476	15	US-10-245-103-51	Sequence 51, Appl
383	50	2.1	50	10	US-09-904-838-205	Sequence 205, App	456	48.2	2.0	3476	15	US-10-245-107-51	Sequence 51, Appl
384	50	2.1	50	10	US-09-906-777-205	Sequence 205, App	457	48.2	2.0	3476	15	US-10-245-143-51	Sequence 51, Appl
385	50	2.1	50	10	US-09-903-603A-205	Sequence 205, App	458	48.2	2.0	3476	15	US-10-245-771-51	Sequence 51, Appl
386	50	2.1	50	10	US-09-904-532-205	Sequence 205, App	459	48.2	2.0	3476	15	US-10-245-851-51	Sequence 51, Appl
387	50	2.1	50	10	US-09-904-766-205	Sequence 205, App	460	48.2	2.0	3476	15	US-10-245-883-51	Sequence 51, Appl
388	50	2.1	50	10	US-09-904-920A-205	Sequence 205, App	461	48.2	2.0	3476	15	US-10-237-535-51	Sequence 51, Appl
389	50	2.1	50	10	US-09-904-877A-205	Sequence 205, App	462	48.2	2.0	3476	15	US-10-238-183-51	Sequence 51, Appl
390	50	2.1	50	10	US-09-903-562-205	Sequence 205, App	463	48.2	2.0	3476	15	US-10-238-283-51	Sequence 51, Appl
391	50	2.1	50	10	US-09-906-618-205	Sequence 205, App	464	48.2	2.0	3476	15	US-10-238-370-51	Sequence 51, Appl
392	50	2.1	50	10	US-09-907-728-205	Sequence 205, App	465	48.2	2.0	3476	15	US-10-245-055-51	Sequence 51, Appl
393	50	2.1	50	11	US-09-904-805-205	Sequence 205, App	466	48.2	2.0	3476	15	US-10-245-147-51	Sequence 51, Appl
394	50	2.1	50	11	US-09-904-938A-205	Sequence 205, App	467	48.2	2.0	3476	15	US-10-245-730-51	Sequence 51, Appl
395	50	2.1	50	11	US-09-906-722A-205	Sequence 205, App	468	48.2	2.0	3476	15	US-10-245-739-51	Sequence 51, Appl
396	50	2.1	50	11	US-09-908-576-205	Sequence 205, App	469	48.2	2.0	3476	15	US-10-246-210-51	Sequence 51, Appl
397	50	2.1	50	13	US-09-903-640-205	Sequence 205, App	470	48.2	2.0	3476	15	US-10-239-196-51	Sequence 51, Appl
398	50	2.1	50	13	US-09-908-093-205	Sequence 205, App	471	48.2	2.0	3476	15	US-10-243-024-51	Sequence 51, Appl
399	50	2.1	50	13	US-09-904-485-205	Sequence 205, App	472	48.2	2.0	3476	15	US-10-243-409-51	Sequence 51, Appl
400	50	2.1	50	13	US-09-905-348-205	Sequence 205, App	473	48.2	2.0	3476	15	US-10-245-621-51	Sequence 51, Appl
401	50	2.1	50	13	US-10-298-993-205	Sequence 205, App	474	48.2	2.0	3476	15	US-10-245-880-51	Sequence 51, Appl
402	50	2.1	50	13	US-10-448-923-205	Sequence 205, App	475	48.2	2.0	3476	15	US-10-245-033-51	Sequence 51, Appl
403	50	2.1	50	15	US-10-299-976-205	Sequence 205, App	476	48.2	2.0	3476	15	US-10-243-095-51	Sequence 51, Appl
404	50	2.1	50	15	US-10-299-937-205	Sequence 205, App	477	48.2	2.0	3476	15	US-10-245-185-51	Sequence 51, Appl
405	50	2.1	50	16	US-10-449-656-205	Sequence 205, App	478	48.2	2.0	3476	15	US-10-245-427-51	Sequence 51, Appl
406	50	2.1	50	16	US-10-448-713-205	Sequence 205, App	479	48.2	2.0	3476	15	US-10-245-770-51	Sequence 51, Appl
407	50	2.1	50	17	US-10-425-447-205	Sequence 205, App	480	48.2	2.0	3476	15	US-10-246-976-51	Sequence 51, Appl
408	50	2.1	50	17	US-10-215-371-205	Sequence 205, App	481	48.2	2.0	3476	15	US-10-243-320-51	Sequence 51, Appl
409	50	2.1	37515	17	US-10-433-793-28	Sequence 28, Appl	482	48.2	2.0	3476	15	US-10-242-743-51	Sequence 51, Appl
410	49.4	2.1	8305	15	US-10-311-455-1542	Sequence 1542, Ap	483	48.2	2.0	3476	15	US-10-242-845-51	Sequence 51, Appl
411	49.4	2.1	47841	17	US-10-433-580-3	Sequence 3, Appli	484	48.2	2.0	3476	15	US-10-237-636-51	Sequence 51, Appl
412	49.4	2.1	73334	17	US-10-311-455-2098	Sequence 2098, Ap	485	48.2	2.0	3476	15	US-10-238-325-51	Sequence 51, Appl
413	49.4	2.1	73334	15	US-10-240-589C-128	Sequence 128, App	486	48.2	2.0	3476	15	US-10-238-411-51	Sequence 51, Appl
414	49.2	2.1	7461	15	US-10-311-455-1757	Sequence 1757, Ap	487	48.2	2.0	3476	15	US-10-243-425-51	Sequence 51, Appl
415	49.2	2.1	21354	13	US-10-221-714A-512	Sequence 512, App	488	48.2	2.0	3476	15	US-10-242-653-51	Sequence 51, Appl
416	49.2	2.1	302250	9	US-09-962-832-154	Sequence 154, App	489	48.2	2.0	3476	15	US-10-243-167-51	Sequence 51, Appl
417	49	2.1	5430	13	US-10-221-714A-14	Sequence 14, Appl	490	48.2	2.0	3476	15	US-10-243-388-51	Sequence 51, Appl
418	49	2.1	6106	13	US-10-221-714A-151	Sequence 151, App	491	48.2	2.0	3476	15	US-10-244-947-51	Sequence 51, Appl
419	49	2.1	6106	15	US-10-311-455-1445	Sequence 1445, Ap	492	48.2	2.0	3476	15	US-10-244-968-51	Sequence 51, Appl
420	49	2.1	6106	17	US-10-257-166-113	Sequence 113, App	493	48.2	2.0	3476	15	US-10-244-990-51	Sequence 51, Appl
421	49	2.1	15767	15	US-10-311-455-1180	Sequence 1180, Ap	494	48.2	2.0	3476	15	US-10-245-079-51	Sequence 51, Appl
422	49	2.1	15767	15	US-10-240-485-106	Sequence 106, App	495	48.2	2.0	3476	15	US-10-245-127-51	Sequence 51, Appl
423	48.8	2.1	9810	15	US-10-311-455-399	Sequence 399, App	496	48.2	2.0	3476	15	US-10-245-207-51	Sequence 51, Appl
424	48.8	2.1	12025	15	US-10-311-455-1272	Sequence 1272, Ap	497	48.2	2.0	3476	15	US-10-245-646-51	Sequence 51, Appl
425	48.8	2.1	13202	15	US-10-311-455-1458	Sequence 1458, Ap	498	48.2	2.0	3476	15	US-10-245-695-51	Sequence 51, Appl
426	48.8	2.1	13712	15	US-10-311-455-1503	Sequence 1503, Ap	499	48.2	2.0	3476	15	US-10-245-699-51	Sequence 51, Appl
427	48.6	2.0	6154	13	US-10-221-613-69	Sequence 69, Appl	500	48.2	2.0	3476	15	US-10-245-737-51	Sequence 51, Appl
428	48.6	2.0	11172	15	US-10-311-455-2026	Sequence 2026, Ap	501	48.2	2.0	3476	15	US-10-245-878-51	Sequence 51, Appl
429	48.6	2.0	17137	15	US-10-311-455-164	Sequence 164, App	502	48.2	2.0	3476	15	US-10-245-890-51	Sequence 51, Appl
430	48.6	2.0	3673778	15	US-10-312-841-1	Sequence 1, Appli	503	48.2	2.0	3476	15	US-10-245-899-51	Sequence 51, Appl
431	48.4	2.0	643	13	US-10-424-599-106363	Sequence 106363,	504	48.2	2.0	3476	15	US-10-247-058-51	Sequence 51, Appl
432	48.4	2.0	6775	17	US-10-433-793-190	Sequence 190, App	505	48.2	2.0	3476	15	US-10-238-261-51	Sequence 51, Appl
433	48.4	2.0	640681	9	US-09-790-988-1	Sequence 1, Appli	506	48.2	2.0	3476	15	US-10-238-324-51	Sequence 51, Appl
434	48.2	2.0	334	15	US-10-029-386-26472	Sequence 26472, A	507	48.2	2.0	3476	15	US-10-241-860-51	Sequence 51, Appl
435	48.2	2.0	538	15	US-10-029-386-12772	Sequence 12772, A	508	48.2	2.0	3476	15	US-10-242-172-51	Sequence 51, Appl
436	48.2	2.0	972	9	US-09-764-853-156	Sequence 156, App	509	48.2	2.0	3476	15	US-10-242-652-51	Sequence 51, Appl
437	48.2	2.0	1720	9	US-09-981-876-53	Sequence 53, Appl	510	48.2	2.0	3476	15	US-10-242-990-51	Sequence 51, Appl
438	48.2	2.0	1720	10	US-09-148-545-53	Sequence 53, Appl	511	48.2	2.0	3476	15	US-10-243-023-51	Sequence 51, Appl
439	48.2	2.0	2013	10	US-09-759-130B-330	Sequence 330, App	512	48.2	2.0	3476	15	US-10-243-103-51	Sequence 51, Appl
440	48.2	2.0	2013	15	US-10-189-123-60	Sequence 60, Appl	513	48.2	2.0	3476	15	US-10-243-276-51	Sequence 51, Appl
441	48.2	2.0	2013	15	US-10-188-495-60	Sequence 60, Appl	514	48.2	2.0	3476	15	US-10-243-364-51	Sequence 51, Appl
442	48.2	2.0	2013	17	US-10-741-790-330	Sequence 330, App	515	48.2	2.0	3476	15	US-10-243-494-51	Sequence 51, Appl
443	48.2	2.0	2558	10	US-09-983-000A-13	GENERAL INFORMATI	516	48.2	2.0	3476	15	US-10-243-494-51	Sequence 51, Appl
444	48.2	2.0	2694	15	US-10-050-704-40	Sequence 40, Appl	517	48.2	2.0	3476	15	US-10-242-172-51	Sequence 51, Appl
445	48.2	2.0	2694	17	US-10-798-512-40	Sequence 40, Appl	518	48.2	2.0	3476	15	US-10-242-652-51	Sequence 51, Appl
446	48.2	2.0	2730	10	US-09-759-130B-329	Sequence 329, App	519	48.2	2.0	3476	15	US-10-242-990-51	Sequence 51, Appl
447	48.2	2.0	2730	15	US-10-189-123-59	Sequence 59, Appl	520	48.2	2.0	3476	15	US-10-243-023-51	Sequence 51, Appl
448	48.2	2.0	2730	15	US-10-188-495-59	Sequence 59, Appl	521	48.2	2.0	3476	15	US-10-243-103-51	Sequence 51, Appl
449	48.2	2.0	2730	17	US-10-741-790-329	Sequence 329, App	522	48.2	2.0	3476	15	US-10-243-276-51	Sequence 51, Appl
450	48.2	2.0	2878	13	US-10-453-420-7	Sequence 7, Appli	523	48.2	2.0	3476	15	US-10-243-364-51	Sequence 51, Appl
451	48.2	2.0	2878	16	US-10-295-027-259	Sequence 259, App	524	48.2	2.0	3476	15	US-10-243-364-51	Sequence 51, Appl
452	48.2	2.0	3438	13	US-10-312-352-60	Sequence 60, Appl	525	48.2	2.0	3476	15	US-10-243-494-51	Sequence 51, Appl

526	48.2	2.0	3476	15	US-10-244-995-51	Sequence 51, Appl	599	46.8	2.0	3153	10	US-09-759-130B-343	Sequence 343, App
527	48.2	2.0	3476	15	US-10-245-230-51	Sequence 51, Appl	600	46.8	2.0	3153	15	US-10-189-123-73	Sequence 73, Appl
528	48.2	2.0	3476	15	US-10-245-253-51	Sequence 51, Appl	601	46.8	2.0	3153	15	US-10-188-495-73	Sequence 73, Appl
529	48.2	2.0	3476	15	US-10-245-479-51	Sequence 51, Appl	602	46.8	2.0	3153	17	US-10-741-790-343	Sequence 343, App
530	48.2	2.0	3476	15	US-10-245-499-51	Sequence 51, Appl	c 603	46.8	2.0	5987	15	US-10-311-455-1536	Sequence 1536, Ap
531	48.2	2.0	3476	15	US-10-245-772-51	Sequence 51, Appl	c 604	46.8	2.0	5987	17	US-10-433-793-132	Sequence 132, App
532	48.2	2.0	3476	15	US-10-245-811-51	Sequence 51, Appl	c 605	46.8	2.0	6301	15	US-10-311-455-25	Sequence 25, Appl
533	48.2	2.0	3476	15	US-10-245-812-51	Sequence 51, Appl	606	46.8	2.0	9760	13	US-10-221-613-114	Sequence 114, App
534	48.2	2.0	3476	15	US-10-245-852-51	Sequence 51, Appl	c 607	46.8	2.0	12968	13	US-10-221-714A-506	Sequence 506, App
535	48.2	2.0	3476	15	US-10-245-875-51	Sequence 51, Appl	c 608	46.8	2.0	12968	15	US-10-239-676-202	Sequence 202, App
536	48.2	2.0	3476	15	US-10-245-881-51	Sequence 51, Appl	c 609	46.8	2.0	12968	15	US-10-311-455-2058	Sequence 2058, Ap
537	48.2	2.0	3476	15	US-10-245-911-51	Sequence 51, Appl	c 610	46.8	2.0	12968	15	US-10-240-453-298	Sequence 298, App
538	48.2	2.0	3476	15	US-10-245-913-51	Sequence 51, Appl	611	46.6	2.0	960	15	US-10-198-846-6381	Sequence 6381, Ap
539	48.2	2.0	3476	15	US-10-246-080-51	Sequence 51, Appl	612	46.6	2.0	2747	9	US-09-917-800A-1588	Sequence 1588, Ap
540	48.2	2.0	3476	15	US-10-246-121-51	Sequence 51, Appl	613	46.6	2.0	5163	15	US-10-311-455-1221	Sequence 1221, Ap
541	48.2	2.0	3476	15	US-10-246-305-51	Sequence 51, Appl	614	46.6	2.0	7676	15	US-10-240-485-151	Sequence 151, App
542	48.2	2.0	3476	15	US-10-246-929-51	Sequence 51, Appl	c 615	46.6	2.0	9180	15	US-10-311-455-1937	Sequence 1937, Ap
543	48.2	2.0	3476	15	US-10-247-036-51	Sequence 51, Appl	c 616	46.6	2.0	10891	15	US-10-311-455-438	Sequence 438, App
544	48.2	2.0	3476	15	US-10-243-255-51	Sequence 51, Appl	c 617	46.6	2.0	11092	15	US-10-311-455-1485	Sequence 1485, Ap
545	48.2	2.0	3476	15	US-10-245-810-51	Sequence 51, Appl	c 618	46.6	2.0	12507	15	US-10-311-455-271	Sequence 271, App
546	48.2	2.0	3476	15	US-10-245-910-51	Sequence 51, Appl	619	46.6	2.0	15548	15	US-10-311-455-2128	Sequence 2128, Ap
547	48.2	2.0	3476	15	US-10-246-098-51	Sequence 51, Appl	c 620	46.6	2.0	40862	15	US-10-311-455-2046	Sequence 2046, Ap
548	48.2	2.0	3476	15	US-10-237-496-51	Sequence 51, Appl	c 621	46.4	2.0	4172	15	US-10-311-455-687	Sequence 687, App
549	48.2	2.0	3476	15	US-10-242-074-51	Sequence 51, Appl	622	46.4	2.0	6040	15	US-10-204-708-70	Sequence 70, Appl
550	48.2	2.0	3476	15	US-10-242-505-51	Sequence 51, Appl	623	46.4	2.0	6040	17	US-10-240-589C-110	Sequence 110, App
551	48.2	2.0	3476	15	US-10-242-574-51	Sequence 51, Appl	624	46.4	2.0	16228	13	US-10-221-613-387	Sequence 387, App
552	48.2	2.0	3476	15	US-10-243-261-51	Sequence 51, Appl	c 625	46.4	2.0	17594	15	US-10-311-455-1999	Sequence 1999, Ap
553	48.2	2.0	3476	15	US-10-243-282-51	Sequence 51, Appl	c 626	46.4	2.0	19131	13	US-10-221-714A-442	Sequence 442, App
554	48.2	2.0	3476	15	US-10-243-402-51	Sequence 51, Appl	c 627	46.2	1.9	471	13	US-10-424-599-112213	Sequence 112213,
555	48.2	2.0	3476	15	US-10-243-431-51	Sequence 51, Appl	c 628	46.2	1.9	5880	13	US-10-221-714A-53	Sequence 53, Appl
556	48.2	2.0	3476	15	US-10-244-164-51	Sequence 51, Appl	c 629	46.2	1.9	5880	15	US-10-240-453-51	Sequence 51, Appl
557	48.2	2.0	3476	15	US-10-244-972-51	Sequence 51, Appl	c 630	46.2	1.9	5881	15	US-10-311-455-1736	Sequence 1736, Ap
558	48.2	2.0	3476	15	US-10-197-942-51	Sequence 51, Appl	c 631	46.2	1.9	6831	15	US-10-311-455-1460	Sequence 1460, Ap
559	48.2	2.0	3476	15	US-10-238-196-51	Sequence 51, Appl	c 632	46.2	1.9	12507	15	US-10-311-455-272	Sequence 272, App
560	48.2	2.0	3476	15	US-10-245-013-51	Sequence 51, Appl	c 633	46.2	1.9	15743	15	US-10-240-453-270	Sequence 270, App
c 561	48.2	2.0	5430	15	US-10-091-438-279	Sequence 279, App	c 634	46.2	1.9	19380	13	US-10-221-613-390	Sequence 390, App
c 562	48.2	2.0	6106	13	US-10-221-714A-151	Sequence 151, App	635	46	1.9	3057	15	US-10-349-680-148	Sequence 148, App
c 563	48.2	2.0	6106	15	US-10-311-455-1445	Sequence 1445, Ap	c 636	46	1.9	4661	17	US-10-433-793-51	Sequence 51, Appl
c 564	48.2	2.0	6106	17	US-10-257-166-113	Sequence 113, App	c 637	46	1.9	6113	15	US-10-204-708-13	Sequence 13, Appl
c 565	48.2	2.0	9646	13	US-10-462-261-1	Sequence 1, Appli	c 638	46	1.9	6113	15	US-10-311-455-403	Sequence 403, App
c 566	48	2.0	5362	15	US-10-240-453-288	Sequence 288, App	c 639	46	1.9	6113	17	US-10-240-589C-13	Sequence 13, Appl
c 567	47.8	2.0	650	13	US-10-027-632-231715	Sequence 231715,	c 640	46	1.9	9095	17	US-10-433-793-92	Sequence 92, Appl
c 568	47.8	2.0	650	13	US-10-027-632-231716	Sequence 231716,	641	46	1.9	9524	15	US-10-311-455-812	Sequence 812, App
c 569	47.8	2.0	650	13	US-10-027-632-231717	Sequence 231717,	642	46	1.9	9524	17	US-10-257-166-76	Sequence 76, Appl
c 570	47.8	2.0	650	16	US-10-027-632-231715	Sequence 231715,	c 643	46	1.9	14316	13	US-10-221-613-408	Sequence 408, App
c 571	47.8	2.0	650	16	US-10-027-632-231716	Sequence 231716,	644	46	1.9	15587	13	US-10-221-613-198	Sequence 198, App
c 572	47.8	2.0	650	16	US-10-027-632-231717	Sequence 231717,	645	46	1.9	16217	15	US-10-311-455-598	Sequence 598, App
c 573	47.6	2.0	9965	15	US-10-311-455-1500	Sequence 1500, Ap	c 646	45.8	1.9	21537	15	US-10-311-455-1971	Sequence 1971, Ap
574	47.6	2.0	12578	13	US-10-221-714A-382	Sequence 382, App	647	45.8	1.9	5520	15	US-10-311-455-1491	Sequence 1491, Ap
575	47.6	2.0	12781	13	US-10-221-714A-107	Sequence 107, App	c 648	45.8	1.9	5659	15	US-10-172-086-31	Sequence 31, Appl
576	47.6	2.0	12781	17	US-10-240-589C-37	Sequence 37, Appl	c 649	45.8	1.9	5659	15	US-10-311-455-347	Sequence 347, App
577	47.4	2.0	40862	15	US-10-311-455-2046	Sequence 2046, Ap	c 650	45.8	1.9	5659	15	US-10-240-485-39	Sequence 39, Appl
578	47.4	2.0	161671	15	US-10-017-117-1	Sequence 1, Appli	c 651	45.8	1.9	5659	17	US-10-311-507-13	Sequence 13, Appl
c 579	47.2	2.0	960	15	US-10-198-846-6381	Sequence 6381, Ap	c 652	45.8	1.9	6065	15	US-10-311-455-478	Sequence 478, App
580	47.2	2.0	5413	13	US-10-221-714A-418	Sequence 418, App	653	45.8	1.9	6072	15	US-10-311-455-3	Sequence 3, Appli
581	47.2	2.0	6074	15	US-10-240-453-248	Sequence 248, App	654	45.8	1.9	6120	15	US-10-311-455-466	Sequence 466, App
c 582	47.2	2.0	6174	13	US-10-221-714A-155	Sequence 155, App	655	45.8	1.9	6361	15	US-10-311-455-1113	Sequence 1113, App
583	47.2	2.0	6191	15	US-10-311-455-1189	Sequence 1189, Ap	c 656	45.8	1.9	7498	15	US-10-311-455-230	Sequence 230, App
c 584	47.2	2.0	7669	15	US-10-311-455-601	Sequence 601, App	c 657	45.8	1.9	18218	15	US-10-311-455-1922	Sequence 1922, Ap
c 585	47.2	2.0	17137	15	US-10-311-455-164	Sequence 164, App	c 658	45.8	1.9	319608	16	US-10-147-603-1	GENERAL INFORMATI
586	47.2	2.0	17144	13	US-10-221-714A-387	Sequence 387, App	c 659	45.6	1.9	6265	9	US-09-129-112-3	Sequence 3, Appli
587	47.2	2.0	513509	10	US-09-754-853A-4	Sequence 4, Appli	c 660	45.6	1.9	11155	15	US-10-311-455-577	Sequence 577, App
c 588	47	2.0	4045	13	US-10-221-714A-466	Sequence 466, App	c 661	45.4	1.9	343	13	US-10-424-599-89995	Sequence 89995, A
589	47	2.0	5006	9	US-09-837-751-7	Sequence 7, Appli	662	45.4	1.9	628	13	US-10-027-632-113152	Sequence 113152,
c 590	47	2.0	7057	13	US-10-221-613-317	Sequence 317, App	663	45.4	1.9	628	16	US-10-027-632-113152	Sequence 113152,
c 591	47	2.0	7057	13	US-10-221-714A-323	Sequence 323, App	664	45.4	1.9	6265	9	US-09-129-112-3	Sequence 3, Appli
c 592	47	2.0	7057	15	US-10-311-455-1821	Sequence 1821, Ap	665	45.4	1.9	7498	15	US-10-311-455-230	Sequence 230, App
c 593	47	2.0	7057	15	US-10-240-485-147	Sequence 147, App	c 666	45.4	1.9	9881	15	US-10-240-452-54	Sequence 54, Appl
c 594	47	2.0	11964	17	US-10-433-793-55	Sequence 55, Appl	c 667	45.4	1.9	10279	15	US-10-311-455-1564	Sequence 1564, Ap
c 595	47	2.0	16258	17	US-10-257-166-120	Sequence 120, App	c 668	45.4	1.9	10279	17	US-10-240-589C-86	Sequence 86, Appl
c 596	47	2.0	172569	13	US-10-087-192-1366	Sequence 1366, Ap	c 669	45.4	1.9	11260	15	US-10-239-676-20	Sequence 20, Appl
597	46.8	2.0	319	10	US-09-814-353-6115	Sequence 6115, Ap	c 670	45.4	1.9	11260	15	US-10-240-453-28	Sequence 28, Appl
598	46.8	2.0	319	10	US-09-814-353-12394	Sequence 12394, A	c 671	45.4	1.9	11996	15	US-10-240-485-46	Sequence 46, Appl

672	45.4	1.9	13420	15	US-10-311-455-890	Sequence 890, App	745	44.2	1.9	9515	15	US-10-240-453-182	Sequence 182, App
673	45.4	1.9	40324	17	US-10-433-793-179	Sequence 179, App	746	44.2	1.9	11187	15	US-10-240-453-326	Sequence 326, App
674	45.2	1.9	1109	13	US-10-424-599-134182	Sequence 134182, A	747	44.2	1.9	18283	13	US-10-221-613-325	Sequence 325, App
c 675	45.2	1.9	2432	15	US-10-198-846-12893	Sequence 12893, A	c 748	44.2	1.9	33053	17	US-10-433-793-36	Sequence 36, Appl
c 676	45.2	1.9	5267	17	US-10-433-793-73	Sequence 73, Appl	c 749	44.2	1.9	198522	13	US-10-087-192-244	Sequence 244, App
c 677	45.2	1.9	8876	15	US-10-311-455-2049	Sequence 2049, Ap	c 750	44	1.9	419	9	US-09-960-352-11234	Sequence 11234, A
c 678	45.2	1.9	17183	15	US-10-311-455-460	Sequence 460, App	c 751	44	1.9	3007	15	US-10-239-676-219	Sequence 219, App
c 679	45.2	1.9	17419	15	US-10-311-455-100	Sequence 100, App	c 752	44	1.9	3007	15	US-10-240-453-319	Sequence 319, App
c 680	45.2	1.9	17419	15	US-10-311-455-1268	Sequence 1268, Ap	c 753	44	1.9	3151	17	US-10-433-793-174	Sequence 174, App
c 681	45.2	1.9	17419	15	US-10-240-453-112	Sequence 112, App	c 754	44	1.9	5820	15	US-10-311-455-511	Sequence 511, App
682	45	1.9	535	17	US-10-021-323-1934	Sequence 1934, Ap	c 755	44	1.9	6129	13	US-10-221-613-108	Sequence 108, App
683	45	1.9	12142	15	US-10-311-455-1646	Sequence 1646, Ap	c 756	44	1.9	6223	13	US-10-221-613-135	Sequence 135, App
c 684	45	1.9	14987	15	US-10-311-455-603	Sequence 603, App	c 757	44	1.9	6306	15	US-10-239-676-129	Sequence 129, App
685	45	1.9	18133	15	US-10-311-455-914	Sequence 914, App	c 758	44	1.9	6437	15	US-10-311-455-1233	Sequence 1233, Ap
686	45	1.9	18133	17	US-10-257-166-100	Sequence 100, App	c 759	44	1.9	7321	13	US-10-221-613-299	Sequence 299, App
687	45	1.9	19659	15	US-10-311-455-739	Sequence 739, App	c 760	44	1.9	7522	15	US-10-311-455-887	Sequence 887, App
c 688	44.8	1.9	4661	17	US-10-433-793-52	Sequence 52, Appl	c 761	44	1.9	7597	15	US-10-311-455-986	Sequence 986, App
c 689	44.8	1.9	5593	15	US-10-311-455-1134	Sequence 1134, Ap	c 762	44	1.9	11964	17	US-10-433-793-56	Sequence 167, App
690	44.8	1.9	6759	15	US-10-311-455-711	Sequence 711, App	c 763	44	1.9	13627	17	US-10-433-793-5	Sequence 5, Appli
c 691	44.8	1.9	7231	15	US-10-240-452-23	Sequence 23, Appl	c 764	44	1.9	13627	17	US-10-433-793-5	Sequence 5, Appli
692	44.8	1.9	10048	17	US-10-433-793-45	Sequence 45, Appl	c 765	44	1.9	17674	15	US-10-311-455-1318	Sequence 1318, Ap
c 693	44.8	1.9	20579	17	US-10-433-793-104	Sequence 104, App	c 766	44	1.9	56153	13	US-10-221-714A-520	Sequence 520, App
694	44.6	1.9	641	13	US-10-027-632-113326	Sequence 113326,	c 767	44	1.9	95109	17	US-10-433-287-80	Sequence 80, Appl
695	44.6	1.9	641	16	US-10-027-632-113326	Sequence 113326,	768	43.8	1.8	449	13	US-10-085-783A-30386	Sequence 30386, A
c 696	44.6	1.9	5979	15	US-10-239-676-18	Sequence 18, Appl	769	43.8	1.8	449	16	US-10-242-535A-30386	Sequence 30386, A
c 697	44.6	1.9	5979	15	US-10-240-453-26	Sequence 26, Appl	770	43.8	1.8	5487	15	US-10-311-455-1571	Sequence 1571, Ap
c 698	44.6	1.9	6063	15	US-10-240-453-268	Sequence 268, App	771	43.8	1.8	6127	15	US-10-240-485-1	Sequence 1, Appli
c 699	44.6	1.9	6759	15	US-10-311-455-712	Sequence 712, App	c 772	43.8	1.8	6233	13	US-10-221-714A-219	Sequence 219, App
c 700	44.6	1.9	13784	17	US-10-257-166-143	Sequence 143, App	c 773	43.8	1.8	6418	13	US-10-221-613-30	Sequence 30, Appl
c 701	44.6	1.9	14649	15	US-10-239-676-121	Sequence 121, App	c 774	43.8	1.8	6418	15	US-10-311-455-296	Sequence 296, App
c 702	44.6	1.9	14649	15	US-10-240-453-141	Sequence 141, App	c 775	43.8	1.8	6811	15	US-10-240-485-94	Sequence 94, Appl
703	44.6	1.9	16236	15	US-10-311-455-995	Sequence 995, App	c 776	43.8	1.8	8227	17	US-10-433-793-156	Sequence 156, App
c 704	44.6	1.9	18283	13	US-10-221-613-326	Sequence 326, App	c 777	43.8	1.8	11996	15	US-10-240-485-45	Sequence 45, Appl
c 705	44.6	1.9	96589	12	US-09-997-722-46	Sequence 46, Appl	c 778	43.8	1.8	12237	15	US-10-311-455-2331	Sequence 2331, Ap
706	44.6	1.9	159400	17	US-10-450-826-33	Sequence 33, Appl	c 779	43.8	1.8	14861	13	US-10-221-613-161	Sequence 161, App
707	44.4	1.9	388	10	US-09-814-353-17525	Sequence 1, Appli	c 780	43.8	1.8	14861	15	US-10-311-455-1167	Sequence 1167, Ap
c 708	44.4	1.9	3410	15	US-10-196-063-1	Sequence 2075, Ap	c 781	43.8	1.8	14919	13	US-10-221-714A-228	Sequence 228, App
c 709	44.4	1.9	4993	15	US-10-311-455-2075	Sequence 1639, Ap	c 782	43.8	1.8	15743	15	US-10-240-453-269	Sequence 269, App
710	44.4	1.9	5798	15	US-10-311-455-1639	Sequence 793, App	c 783	43.8	1.8	16724	15	US-10-311-455-1063	Sequence 1063, Ap
c 711	44.4	1.9	6123	15	US-10-311-455-793	Sequence 28, Appl	c 784	43.8	1.8	16724	15	US-10-240-485-89	Sequence 89, Appl
712	44.4	1.9	6239	13	US-10-221-613-28	Sequence 40, Appl	c 785	43.8	1.8	17703	17	US-10-257-166-33	Sequence 33, Appl
713	44.4	1.9	7168	17	US-10-240-589C-40	Sequence 372, App	c 786	43.8	1.8	18154	15	US-10-311-455-227	Sequence 227, App
c 714	44.4	1.9	8032	13	US-10-221-613-372	Sequence 1541, Ap	c 787	43.8	1.8	18154	15	US-10-311-455-227	Sequence 227, App
715	44.4	1.9	8305	15	US-10-311-455-1541	Sequence 21, Appl	788	43.6	1.8	818	13	US-10-027-632-131730	Sequence 131730,
c 716	44.4	1.9	11049	15	US-10-204-708-21	Sequence 641, App	789	43.6	1.8	818	16	US-10-027-632-131730	Sequence 131730,
c 717	44.4	1.9	11049	15	US-10-311-455-641	Sequence 27, Appl	790	43.6	1.8	1988	9	US-09-864-761-10234	Sequence 10234, A
c 718	44.4	1.9	11049	17	US-10-240-589C-27	Sequence 422, App	c 791	43.6	1.8	5368	15	US-10-311-455-2149	Sequence 2149, Ap
719	44.4	1.9	11694	13	US-10-221-714A-422	Sequence 325, App	c 792	43.6	1.8	5407	15	US-10-311-455-2064	Sequence 2064, Ap
c 720	44.4	1.9	18283	13	US-10-221-613-325	Sequence 90, Appl	c 793	43.6	1.8	5511	15	US-10-311-455-1843	Sequence 1843, Ap
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Job time : 1055 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 16, 2004, 23:06:58 ; Search time 4656 Seconds
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Searched: 3470272 seqs, 21671516995 residues 6940544
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

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AF127670
LOCUS AF127670 1285 bp mRNA linear PRI 13-OCT-2000
DEFINITION Homo sapiens hyaluronic acid receptor (HAR) mRNA, complete cds.
ACCESSION AF127670
VERSION AF127670.2 GI:10800121
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1285)
AUTHORS Winkelmann,J.C., Basu,S., Ozdemir,E. and Blough,R.I.
TITLE HAR: a novel homolog of CD44 and putative hyaluronic acid receptor encoded by a gene on human chromosome 11p15
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1009)
AUTHORS Winkelmann,J.C., Basu,S., Ozdemir,E. and Blough,R.I.
TITLE Direct Submission
JOURNAL Submitted (11-FEB-1999) Hematology-Oncology, University of Cincinnati, 231 Bethesda Avenue, Cincinnati, Ohio 45267-0508, USA
REFERENCE 3 (bases 1 to 1285)
AUTHORS Winkelmann,J.C., Basu,S., Ozdemir,E. and Blough,R.I.
TITLE Direct Submission
JOURNAL Submitted (12-OCT-1999) Hematology-Oncology, University of Cincinnati, 231 Bethesda Avenue, Cincinnati, Ohio 45267-0508, USA
REMARK Sequence update by submitter
COMMENT On Oct 13, 2000 this sequence version replaced gi:5732667.
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source

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RESULT 2

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LOCUS

DEFINITION

AX136227

ACCESSION

AX136227.1

VERSION

KEYWORDS

SOURCE

ORGANISM

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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS

Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.

Secretory protein or membrane protein

Patent: EP 1067182-A 149 10-JAN-2001;

Helix Research Institute (JP)

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Sequence 149 from Patent EPI067182.

AX136227 GI:14272635

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VERSION BD123566.1 GI:23218511
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REFERENCE 1 (bases 1 to 1755)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: JP 2002017376-A 75 22-JAN-2002;
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PN JP 2002017376-A/75
PD 22-JAN-2002
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PI SUGIYAMA,
PI KOJI HAYASHI
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QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 621 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAACA 680
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 681 GAAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 740
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 741 CCTACTACTCTCCTCGTCCAGCTTCCACTTCTTAFTCCACGGAGAAAAAATTGATT 800
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
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QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 861 GAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 920
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 921 CTAGTGCTTGCTCTCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGTATGTCAA 980
QY 261 ArgTyrValLysAlaPhePropheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 981 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC 1040
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Db 1041 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCTTAATGAGGAATCAAGAAAAACT 1100
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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QY 321 GluVal 322
Db 1161 GAAGTT 1166

RESULT 4
AK075443
LOCUS
DEFINITION
Homo sapiens cdNA PSEC0135 fis, clone PLACE1004850, highly similar
to Homo sapiens lymphatic endothelium-specific hyaluronan receptor
LYVE-1 mRNA.
AK075443 1755 bp mRNA linear PRI 03-SEP-2002

ACCESSION AK075443
VERSION AK075443.1 GI:22761535
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K.,
Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T.,
Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.
HRI human cDNA sequencing project
Unpublished
2 (bases 1 to 1755)
Isogai,T. and Yamamoto,J.
Direct Submission
Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass
sequencing, clone selection and full insert sequencing: Helix
Research Institute (supported by Japan Key Technology Center etc.);
cDNA library construction: Institute of Medical Science, University
Of Tokyo, Laboratory of Genome Structure, Human Genome Center.
FEATURES
Location/Qualifiers
1..1755
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1004850"
/tissue_type="placenta"
/clone_lib="PLACE1"
/note="cloning vector: pME18SFL3"
ORIGIN

Alignment Scores:
Pred. No.: 2.42e-127 Length: 1755
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-063-670-6 (1-322) x AK075443 (1-1755)
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QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 261 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCATCCAGGTGTCTATGCAGAATTATGGGG 320
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 321 ATCACCCCTTGTGACAAAAAGGCGAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 380
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 381 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 440
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 441 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTCGTGCATCTCTAGGATT 500
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 501 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCCTGATTTGGAAGGTTCCAGTG 560
QY 121 SerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 561 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 620

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2029)
AUTHORS Lal,P., Tang,Y.T., Gorgone,G.A., Corley,N.C., Guegler,K.J.,
Baughn,M.R., Akerblom,I.E., Young,J.A., Yue,H., Patterson,C.,
Reddy,R., Hillman,J.L. and Bandman,O.
TITLE Human signal peptide-containing protein
JOURNAL Patent: JP 2002519030-A 64 02-JUL-2002;
INCYTE PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002519030-A/64
PD 02-JUL-2002
PF 25-JUN-1999 JP 2000557363
PR 26-JUN-1998 US 60/090762,31-JUL-1998 US 60/094983 PR
01-OCT-1998 US 60/102686,11-DEC-1998 US 60/112129 PI PREETI
LAL,Y TOM TANG,GINA A GORGONE,NEIL C CORLEY,KARL J PI GUEGLER,
PI MARIAH R BAUGHN,INGRID E AKERBLOM,JANICE AU YOUNG,HENRY YUE,
PI CHANDRA PATTERSON,ROOPA REDDY,JENNIFER L HILLMAN,OLGA BANDMAN
PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61P9/00,A61P15/00,
PC A61P25/00,
PC A61P29/00,A61P35/00,A61P43/00,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/68//C12P21/08, PC
C12N15/00,
PC A61K37/02,C12N5/00
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FH Key Location/Qualifiers
FT source 1..2029
FT /organism='Homo sapiens (human)'.
FEATURES
source Location/Qualifiers
1..2029
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 2.92e-127 Length: 2029
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 243 GTCCAAGGCTCTTGGCTGCAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 302
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 303 ATCACCCCTTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTTCACAGAGCTAAGGAGGCC 362
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 363 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAACAGCCTTGAAAGCT 422
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db 423 AGCTTTGAAGCTTGACGCTATGGCTGGGTGGAGATGGATTCGTGCTCATCTCTAGGATT 482
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuLeuTrpLysValProVal 120
Db 483 AGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG 542
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

Db 543 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACCTTGGACTAACTCGTGCAATT 602
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 603 CCAGAAATTATCACCCAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 662
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 843 GAAATAAAGCAGCAATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 902
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 903 CTAGTGCTTGCTCTCCTCTCTTTTGGTGTCTGCAGCTGGTCTTGGATTTTGTATGTCAA 962
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 963 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGAAATGATCGAAACC 1022
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
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QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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QY 321 GluVal 322
Db 1143 GAAGTT 1148
RESULT 7
AR410761
LOCUS AR410761 2372 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 200 from patent US 6635468.
ACCESSION AR410761
VERSION AR410761.1 GI:40162261
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2372)
Ashkenazi,A., Botstein,D., Desnovers,L., Eaton,D.L., Ferrara,N.,
Filvaroff,E., Fong,S., Gao,W.-Q., Gerber,H., Gerritsen,M.E.,
Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J.,
Kl javin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A.,
Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: US 6635468-A 200 21-OCT-2003;
FEATURES Location/Qualifiers
source 1..2372
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 3.56e-127 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match:	100.00%	Indels:	0
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QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCAAGGCTCTTTGGGTGCAGAAAGAGCTTCCATCCAGGTGTCAATGCAGAATTATGGGG	279
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCCCTTGTGAGCAAAAAGCGGAACACGACGCTGAATTTACAGAAAGCTAAGGAGGCC	339
QY	61	CysArgLeuLeuGlySerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGACCAAGTTGRAACAGCCTTGAAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	460	AGCCCAAACCCCAAGTGTGGGAAAAATGGGTGGTGTCTGATTTGGAAGGTTCCAGTG	519
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCTATGTTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCAAGAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTATTTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	699
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTACTCCTCCTCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT	759
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Db	760	TGTGTACAGAAAGTTTTTATGGAACACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu	240
Db	820	GAAAAATAAAGCAGCATTCCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGGAAGGCCCATGATAGCAACCCCTAATGAGGAATCAAGAAAACT	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAAACCCAGAAAGAGTCCAAAGAGTCCAAGCAAAAACCTACCGTGCATGCTTGGAAAGCT	1119
QY	321	GluVal	322
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RESULT 8	AX092274	2372 bp	DNA	linear	PAT 21-MAR-2001
LOCUS	Sequence 5 from Patent WO0116318.				
DEFINITION	AX092274				
ACCESSION	AX092274.1	GI:13444451			
VERSION					
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1	Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and Wood,W.I.			
AUTHORS	Secreted and transmembrane polypeptides and nucleic acids encoding the same				
TITLE	Patent: WO 0116318-A 5 08-MAR-2001; Genentech, Inc. (US)				
JOURNAL	Location/Qualifiers				
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ORIGIN					
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Pred. No.:	1657.00	Matches:	322		
Score:	100.00%	Conservative:	0		
Percent Similarity:	100.00%	Mismatches:	0		
Best Local Similarity:	100.00%	Indels:	0		
Query Match:	6	Gaps:	0		
DB:					
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Db	220	GTCCAAGGCTCTTTGGGTGCAGAAAGAGCTTTCATCCAGGTGTCAATGCAGAATTATGGGG	279		
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60		
Db	280	ATCACCCCTTGTGAGCAAAAAGCGGAACACGACGCTGAATTTACAGAAAGCTAAGGAGGCC	339		
QY	61	CysArgLeuLeuGlySerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80		
Db	340	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	399		
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100		
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT	459		
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120		
Db	460	AGCCCAAACCCCAAGTGTGGGAAAAATGGGTGGTGTCTGATTTGGAAGGTTCCAGTG	519		
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140		
Db	520	AGCCGACAGTTTGCAGCCTATGTTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT	579		
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160		
Db	580	CCAGAAATTATCACCAAGAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA	639		
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180		
Db	640	GAATTATTTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	699		
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200		
Db	700	CCTACTACTACTCCTCCTCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT	759		
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220		
Db	760	TGTGTACAGAAAGTTTTTATGGAACACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	819		
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu	240		
Db	820	GAAAAATAAAGCAGCATTCCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	879		
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260		
Db	880	CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA	939		
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr	280		
Db	940	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC	999		
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300		
Db	1000	AAAGTAGTAAAGGAGGAGGAAGGCCCATGATAGCAACCCCTAATGAGGAATCAAGAAAACT	1059		
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320		
Db	1060	GATAAAAACCCAGAAAGAGTCCAAAGAGTCCAAGCAAAAACCTACCGTGCATGCTTGGAAAGCT	1119		
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Db 700 CCTACTACTCCTCCTCCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
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QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
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Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAATGATCGAAACC 999
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Db 1000 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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RESULT 9
AX454446
LOCUS
DEFINITION Sequence 31 from Patent WO0208284.
ACCESSION AX454446
VERSION AX454446.1 GI:21713847
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0208284-A 31 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)

FEATURES
source Location/Qualifiers
1. .2372
/organism="Homo sapiens"
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ORIGIN
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Query Match: 100.00% Indels: 0
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US-10-063-670-6 (1-322) x AX454446 (1-2372)

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QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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QY 121 SerArgGlnPheAlaIaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCAAT 579
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LOCUS
DEFINITION Sequence 31 from Patent WO0200690.

AX490924 2372 bp DNA linear PAT 16-AUG-2002

ACCESSION AX490924
VERSION AX490924.1 GI:22323799
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0200690-A 31 03-JAN-2002;
Genentech, Inc. (US)
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source Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 3.56e-127 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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LOCUS AX697609 2372 bp DNA linear PAT 02-APR-2003
DEFINITION Sequence 200 from Patent WO0104311.
ACCESSION AX697609
VERSION AX697609.1 GI:29498705
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Ashkenazi,A.J., Botstein,D., Desnovers,L., Eaton,D.L., Ferrara,N.,
Filvaroff,E., Fong,S., Gao,W.Q., Gerber,H., Gerritsen,M.E.,
Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Hillan,K.J.,
Kl javin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A.,
Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0104311-A 200 18-JAN-2001;
Genentech Inc. (US)
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source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN
Alignment Scores:
Pred. No.: 3.56e-127 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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DB: 6 Gaps: 0
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QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
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Db	340	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgile	100
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LOCUS			
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ACCESSION	BD172392		
VERSION	BD172392.1	GI:28413692	
KEYWORDS	JP 2002223786-A/165.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1	(bases 1 to 2372)	

AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL	Patent: JP 2002223786-A 165 13-AUG-2002;
COMMENT	GENENTECH INC OS Homo sapiens (human) PN JP 2002223786-A/165 PD 13-AUG-2002 PF 18-DEC-2001 JP 2001385135 PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR 17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR 17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR 17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR 18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR 17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR 21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR 24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR 24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063121 PR 24-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR 27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR 28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR 28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR 28-OCT-1997 US 60/063544,28-OCT-1997 US 60/063564 PR 29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR 29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063435 PR 29-OCT-1997 US 60/064215,29-OCT-1997 US 60/063735 PR 29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064103 PR 31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR 07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR 17-NOV-1997 US 60/065846,18-NOV-1997 US 60/065693 PR 21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066364 PR 24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR 24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR 24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI JIAN ZHENG, PI JEAN YUAN PC C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC C12N5/10, PC C12P21/02//C12P21/08,(C12P21/02,C12R1:19),(C12P21/02,C12R1:91), PC (C12P21/02,C12R1:645),C12N15/00,C12N5/00 CC Secreted and transmembrane polypeptides and nucleic CC acids encoding the same -- FH Key Location/Qualifiers FT source 1..2372 /organism='Homo sapiens (human)'. FT Location/Qualifiers 1..2372 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
FEATURES	
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Alignment Scores:	
Pred. No.:	3.56e-127 Length: 2372
Score:	1657.00 Matches: 322
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
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Qy	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAATAAAGCAGCATTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGCTCTG	879
Qy	241	LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCystTyrValLys	260
Db	880	CTAGTGCTTGCTCTCCTCTTCTTTGGTGTCTGCAGCTGGTCTTGATTTTGCTATGTCAA	939
Qy	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCCCTTCCTTTTACAAACAAGAAATCAGCAGAAGGAATGATCGAAACC	999
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Qy	321	GluVal 322	
Db	1120	GAAGTT 1125	
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DEFINITION	Secreted and transmembrane polypeptides and nucleic acids encoding the same.		
ACCESSION	BD173030		
VERSION	BD173030.1	GI:28414336	
KEYWORDS	.JP 2002238587-A/165.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 2372) Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.			
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same			
JOURNAL	Patent: JP 2002238587-A 165 27-AUG-2002; GENENTECH INC			
COMMENT	OS Homo sapiens (human) PN JP 2002238587-A/165 PD 27-AUG-2002 JP 2001385248 PF 18-DEC-2001 JP 60/059115,17-SEP-1997 US 60/059184 PR PR 17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR 17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR 17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR 18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR 17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR 21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR 24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR 24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063121 PR 24-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR 27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR 28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR 28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR 28-OCT-1997 US 60/063544,28-OCT-1997 US 60/063564 PR 29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR 29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063435 PR 29-OCT-1997 US 60/064215,29-OCT-1997 US 60/063735 PR 29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064103 PR 31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR 07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR 17-NOV-1997 US 60/065846,18-NOV-1997 US 60/065693 PR 21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066364 PR 24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR 24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR 24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI JIAN ZHENG, PI JEAN YUAN PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC C12N15/02, PC C12P21/02,C12P21/08/(C12P21/02,C12R1:91),(C12P21/02,C12R1:19), PC (C12P21/02,C12R1:645),C12N15/00,C12N5/00,C12N15/00 CC Secreted and transmembrane polypeptides and nucleic CC acids encoding the same FH Key Location/Qualifiers FT source 1..2372 /organism='Homo sapiens (human)'. FT Location/Qualifiers 1..2372 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"			
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ORIGIN				
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Db 220 GTCCAAGGCTCTTTGGCTGCAGAAAGAGCTTTCCATCCAGGTGTCTATGCAGAAATTATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
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Db 280 ATCACCCCTTGTGAGCAAAAAGCGCAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 339

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Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCTGGTTCATCTCTAGGATT 459

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QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
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QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrVallys 260
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Db 1120 GAAGTT 1125

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2004, 01:23:18 ; Search time 467 Seconds
(without alignments)
2929.164 Million cell updates/sec

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Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 800 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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16	1657	100.0	2372	7	ACA91166	Aca91166 Novel hum
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18	1657	100.0	2372	7	ACA60365	Aca60365 Novel hum
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22	1657	100.0	2372	7	ACA63988	Aca63988 cDNA enco
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24	1657	100.0	2372	7	ACD45151	Acd45151 Human sec
25	1657	100.0	2372	7	ABX96181	Abx96181 Human sec
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27	1657	100.0	2372	7	ACA93699	Aca93699 Human cDN
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35	1657	100.0	2372	7	ACA98450	Aca98450 Human PRO
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37	1657	100.0	2372	8	ACD19807	Acd19807 Human sec
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49	1657	100.0	2372	8	ADA42381	Ada42381 Human sec
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51	1657	100.0	2372	8	ADA00336	Ada00336 Human sec
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55	1657	100.0	2372	8	ADA17304	Ada17304 Human sec
56	1657	100.0	2372	8	ADA42807	Ada42807 Human sec
57	1657	100.0	2372	8	ACD23655	Acd23655 Human PRO
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76	1657	100.0	2372	9	ADC12992	Adc12992 Human sec
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78	1657	100.0	2372	9	ADC52333	Adc52333 Novel hum
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83	1657	100.0	2372	9	ADD03581	Add03581 Human sec	156	199.5	12.0	4674	7	ABX77520	Abx77520 Different
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85	1657	100.0	2372	9	ADD36009	Add36009 Novel hum	158	197	11.9	2387	7	ABX76192	Abx76192 Lung canc
86	1657	100.0	2372	9	ADE34833	Ade34833 Human sec	159	197	11.9	2905	7	ABX63495	Abx63495 Human CDN
87	1657	100.0	2372	10	ADC52143	Adc52143 Novel hum	160	197	11.9	3474	8	ADA10891	Ada10891 Human CDN
88	1657	100.0	2372	10	ADE79278	Ade79278 Human sec	161	191.5	11.6	339	7	ACC43051	Acc43051 Nucleotid
89	1657	100.0	2372	10	ADE79702	Ade79702 Human sec	162	190	11.5	336	7	ACC43049	Acc43049 Nucleotid
90	1657	100.0	2372	10	ADE73378	Ade73378 Human sec	163	188	11.3	336	7	ACC43052	Acc43052 Nucleotid
91	1657	100.0	2372	10	ADE41281	Ade41281 Human sec	164	186	11.2	336	7	ACC43053	Acc43053 Nucleotid
92	1657	100.0	2372	10	ADE73913	Ade73913 Human sec	165	184	11.1	336	7	ACC43054	Acc43054 Nucleotid
93	1654	99.8	2324	4	ABA09223	Aba09223 Human PRO	166	182	11.0	336	7	ACC43050	Acc43050 Nucleotid
94	1651	99.6	2313	2	AAV22687	Aav22687 DNA encod	167	180.5	10.9	2764	5	AAS81254	Aas81254 DNA encod
95	1651	99.6	2369	6	ABL90698	Ab190698 Human pol	168	179	10.8	2273	5	AAS81258	Aas81258 DNA encod
96	1547	93.4	2967	3	AAC59803	Aac59803 Human sec	169	170	10.3	106	4	AAI46523	Aai46523 Probe #15
97	1531	92.4	1680	9	ADD04999	Add04999 Human sec	170	170	10.3	106	6	ABS14478	Abs14478 Human gen
98	1511.5	91.2	1127	7	ACA10111	Aca10111 Human NOV	171	166.5	10.0	399	8	ACH49200	Ach49200 Human leu
99	1103	66.6	1896	4	AAD10132	Aad10132 Mouse lym	172	165	10.0	820	10	ADE71448	Ade71448 Dog cDNA
100	1103	66.6	1896	6	ABL35066	Abl35066 Murine CD	173	158	9.5	549	6	ABZ34973	Abz34973 Human gen
101	901	54.4	596	6	ABT09892	Abt09892 Human bre	174	158	9.5	549	7	ABZ91738	Abz91738 Human nuc
102	803	48.5	716	5	AAF94017	Aaf94017 Primer sp	175	151	9.1	2863	9	ADB62456	Adb62456 Human CDN
103	673	40.6	411	8	ACH20895	Ach20895 Human adu	176	148.5	9.0	425	8	ACH48521	Ach48521 Human leu
104	595.5	35.9	559	10	ADE71446	Ade71446 Rat cDNA	177	145.5	8.8	781	7	ABX74436	Abx74436 Human CDN
105	592	35.7	451	2	AAX41156	Aax41156 Human sec	178	145.5	8.8	1144	7	ABX63446	Abx63446 Human CDN
106	440	26.6	486	8	ACH22904	Ach22904 Human adu	179	145.5	8.8	1144	9	ADE25720	Ade25720 Human CDN
107	386	23.3	279	10	ADE71447	Ade71447 Rat cDNA	180	145.5	8.8	1422	7	ACC72678	Acc72678 Human can
108	306	18.5	469	4	ABA54110	Aba54110 Human foe	181	145.5	8.8	1422	7	ABX76382	Abx76382 Lung canc
109	306	18.5	469	4	AAI333763	Aai333763 Probe #24	182	145.5	8.8	1728	7	ABX63445	Abx63445 Human CDN
110	306	18.5	469	4	ABA23859	Aba23859 Probe #23	183	145	8.8	351	6	ABV95472	Abv95472 Human pan
111	306	18.5	469	4	AAK27829	Aak27829 Human bon	184	145	8.8	1414	2	AAQ27190	Aaq27190 Tumour ne
112	306	18.5	469	4	ABS27409	Abs27409 Human liv	185	145	8.8	1414	2	AAV71778	Aav71778 Tumour ne
113	306	18.5	469	6	ABS02280	Abs02280 Human gen	186	145	8.8	1414	4	AAD06019	Aad06019 Human tum
114	285	17.2	363	2	AAX41003	Aax41003 Human sec	187	145	8.8	1414	6	ABS54635	Abs54635 Human CDN
115	281.5	17.0	457	4	AAI33382	Aai33382 Probe #20	188	144	8.7	3365	7	AAD48132	Aad48132 Rat CD441
116	281.5	17.0	457	6	ABS01959	Abs01959 Human gen	189	143.5	8.7	396	8	ACH30555	Ach30555 Human tes
117	277	16.7	373	2	AAX51631	Aax51631 Human sec	190	142.5	8.6	8444	6	ABT08487	Abt08487 Human nov
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119	233.5	14.1	1089	6	ABN86523	Abn86523 Nucleotid	192	141.5	8.5	8495	6	ABT08488	Abt08488 Human nov
120	231	13.9	2747	6	ABN86507	Abn86507 Rat glyco	193	138.5	8.4	1411	4	AAH23114	Aah23114 Osteoarth
121	231	13.9	2747	6	ABK63681	Abk63681 Rat seque	194	137	8.3	3260	6	ABT08489	Abt08489 Human nov
122	229.5	13.9	1177	6	ABN86522	Abn86522 Nucleotid	195	137	8.3	4576	6	ABA04662	Aba04662 Human Hya
123	224	13.5	3207	2	AAQ14263	Aaq14263 p-meta-1	196	137	8.3	4642	7	ABX13822	Abx13822 cDNA enco
124	223	13.5	1992	6	ABZ35325	Abz35325 Human gen	197	137	8.3	4962	7	ABX13823	Abx13823 cDNA enco
125	222	13.4	141	4	ABA66678	Aba66678 Human foe	198	136	8.2	4706	7	ABA04648	Aba04648 Rat Hyalu
126	222	13.4	141	4	AAI46891	Aai46891 Probe #15	199	136	8.2	4706	7	ABX13821	Abx13821 cDNA enco
127	222	13.4	141	4	ABA33740	Aba33740 Probe #12	200	135.5	8.2	3153	4	AAF29464	Aaf29464 Murine br
128	222	13.4	141	4	AAK40837	Aak40837 Human bon	201	135.5	8.2	3153	7	ACD66770	Acd66770 Secreted
129	222	13.4	141	6	ABS14788	Abs14788 Human liv	202	135.5	8.2	3153	8	ADB90788	Adb90788 Mouse CDN
130	222	13.4	141	6	ABS14788	Abs14788 Human gen	203	133.5	8.1	1734	6	ABS70406	Abs70406 Human bon
131	215	13.0	1354	2	AAQ21185	Aaq21185 Clone CD4	204	132.5	8.0	2160	9	ADB63670	Adb63670 Human CDN
132	215	13.0	1354	2	AAT14724	Aat14724 Human hae	205	131.5	7.9	2652	7	ABZ81727	Abz81727 Rat mutan
133	215	13.0	1354	2	AAV63461	Aav63461 Human CD4	206	131	7.9	2013	4	AAF29460	Aaf29460 Human TAN
134	215	13.0	1354	2	AAV81218	Aav81218 Human CD4	207	131	7.9	2013	7	ACD66767	Acd66767 Secreted
135	215	13.0	1354	3	AAA50597	Aaa50597 Human hae	208	131	7.9	2013	8	ADB90775	Adb90775 Human TAN
136	215	13.0	1354	4	AAS03191	Aas03191 Human hae	209	131	7.9	2730	4	AAF29459	Aaf29459 Human TAN
137	213	12.9	1794	3	AAA52811	Aaa52811 Human CD4	210	131	7.9	2730	7	ACD66766	Acd66766 Secreted
138	213	12.9	1794	6	ABV94385	Abv94385 Breast ca	211	131	7.9	2730	8	ADB90774	Adb90774 Human CDN
139	213	12.9	1794	6	ABK84043	Abk84043 Human cDN	212	131	7.9	3476	4	AAA91017	Aaa91017 Human sec
140	212	12.8	1083	9	ADD90591	Add90591 Human CD4	213	131	7.9	3476	6	ABK69986	Abk69986 cDNA enco
141	212	12.8	1807	7	AAD48131	Aad48131 Human CD4	214	131	7.9	3476	8	ADA01319	Ada01319 Human PRO
142	212	12.8	4365	9	ADE25668	Ade25668 Human cDN	215	131	7.9	3476	8	ADA43748	Ada43748 Human CDN
143	210	12.7	1297	6	ABN86521	Abn86521 Nucleotid	216	131	7.9	3476	8	ADA43516	Ada43516 Human CDN
144	203	12.3	1483	5	AAA91130	Aaa91130 CD44Hextr	217	131	7.9	3476	8	ADA01191	Ada01191 Human PRO
145	202.5	12.2	1468	5	AAA91129	Aaa91129 CD44Hextr	218	131	7.9	3476	8	ADA01075	Ada01075 Human CDN
146	199.5	12.0	1737	6	ABN86520	Abn86520 Nucleotid	219	131	7.9	3476	8	ADA43632	Ada43632 Human CDN
147	199.5	12.0	1824	7	ABZ70446	Abz70446 Human CD4	220	131	7.9	3476	8	ADA06894	Ada06894 Human PRO
148	199.5	12.0	2100	5	AAA91011	Aaa91011 Human CD4	221	131	7.9	3476	8	ADA08382	Ada08382 Novel hum
149	199.5	12.0	2100	9	ADD90593	Add90593 Human CD4	222	131	7.9	3476	8	ADB99675	Adb99675 Human PRO
150	199.5	12.0	2307	4	AAS03192	Aas03192 Human epi	223	131	7.9	3476	8	ADB86958	Adb86958 Human PRO
151	199.5	12.0	2308	2	AAQ21186	Aaq21186 Clone CD4	224	131	7.9	3476	8	ADB66113	Adb66113 Human CDN
152	199.5	12.0	2308	2	AAT14725	Aat14725 Human epi	225	131	7.9	3476	9	ADB99791	Adb99791 Human PRO
153	199.5	12.0	2308	2	AAV63462	Aav63462 Human CD4	226	131	7.9	3476	9	ADB99446	Adb99446 Novel hum
154	199.5	12.0	2308	2	AAV81219	Aav81219 Human CD4	227	131	7.9	3476	9	ADB65997	Adb65997 Human CDN

228	131	7.9	3476	9	ADC23395	Adc23395 Human cDN	301	127.5	7.7	1985	7	ACD02956	Novel hum
229	131	7.9	3476	9	ADC26088	Adc26088 Human PRO	302	127.5	7.7	1985	7	ACD01771	Novel hum
230	131	7.9	3476	9	ADE04915	Ade04915 Human PRO	303	127.5	7.7	1985	7	ACA91963	Novel hum
231	131	7.9	3476	9	ADE11221	Ade11221 Human PRO	304	127.5	7.7	1985	7	ACA60174	Human cDN
232	131	7.9	3476	9	ADD88152	Add88152 Human PRO	305	127.5	7.7	1985	7	ACA89388	cdNA enco
233	131	7.9	3476	9	ADD95447	Add95447 Human cDN	306	127.5	7.7	1985	7	ACA73398	Human sec
234	131	7.9	3476	9	ADE06377	Ade06377 Human PRO	307	127.5	7.7	1985	7	ACA05713	Human sec
235	131	7.9	3476	9	ADE38152	Ade38152 Human PRO	308	127.5	7.7	1985	7	ACA66547	cdNA enco
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239	131	7.9	3476	10	ADE51818	Ade51818 Human cDN	312	127.5	7.7	1985	7	ACD21796	Human sec
240	131	7.9	3476	10	ADE37676	Ade37676 Human cDN	313	127.5	7.7	1985	7	ACF12961	Human sec
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245	131	7.9	3476	10	ADE39443	Ade39443 Human PRO	318	127.5	7.7	1985	7	ACD18155	Human sec
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248	131	7.9	3476	10	ADE19709	Ade19709 Human PRO	321	127.5	7.7	1985	7	ACA70038	Human sec
249	131	7.9	3476	10	ADE77287	Ade77287 Human cDN	322	127.5	7.7	1985	7	ACD12260	Novel hum
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252	131	7.9	3476	10	ADE37915	Ade37915 Human PRO	325	127.5	7.7	1985	7	ACD25371	Novel hum
253	131	7.9	3476	10	ADE64525	Ade64525 Human PRO	326	127.5	7.7	1985	7	ACD17848	Human sec
254	131	7.9	3476	10	ADE38860	Ade38860 Human PRO	327	127.5	7.7	1985	7	ACC88135	Human sec
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257	131	7.9	3476	10	ADE38744	Ade38744 Human PRO	330	127.5	7.7	1985	7	ACH06954	Human sec
258	131	7.9	3476	10	ADE37444	Ade37444 Human cDN	331	127.5	7.7	1985	7	ABX98166	Human cDN
259	131	7.9	3476	10	ADE06261	Ade06261 Human PRO	332	127.5	7.7	1985	7	ABX13917	Human PRO
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261	131	7.9	3476	10	ADE38628	Ade38628 Human PRO	334	127.5	7.7	1985	7	ACC88442	Human sec
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263	131	7.9	3476	10	ADD89164	Add89164 Human PRO	336	127.5	7.7	1985	7	ABX75554	Human cDN
264	131	7.9	3476	10	ADD88931	Add88931 Human PRO	337	127.5	7.7	1985	7	ABX97757	Human PRO
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266	131	7.9	3476	10	ADE77403	Ade77403 Human cDN	339	127.5	7.7	1985	7	ACA57696	Human PRO
267	131	7.9	3476	10	ADE65279	Ade65279 Human PRO	340	127.5	7.7	1985	7	ACD14224	Human PRO
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269	131	7.9	3476	10	ADE38512	Ade38512 Human cDN	342	127.5	7.7	1985	7	ACC88749	Human sec
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274	129.5	7.8	1522	3	AAA57363	Aaa57363 DNA encod	347	127.5	7.7	1985	7	ACC86412	Human sec
275	129.5	7.8	6761	3	AAA57362	Aaa57362 DNA encod	348	127.5	7.7	1985	7	ACC89670	Human sec
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293	127.5	7.7	1985	7	ACC89363	Acc89363 Human sec	366	127.5	7.7	1985	7	ACA70345	Human sec
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756	126.5	7.7	2465	6	ABK62593	Abk62593	Rat seque
757	125	7.5	2753	9	ADB47730	Adb47730	Novel hum
758	125	7.5	1414	6	ABL68341	Ab168341	Kidney ca
759	125	7.5	1414	6	ABK83989	Abk83989	Human cdn
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771	113.5	6.8	285	3	AAA63526	Aaa63526	DNA encod
772	113	6.8	2087	6	ABA02881	Aba02881	Human ver
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774	113	6.8	8224	2	AAQ12261	Aaq12261	Versican
775	113	6.8	8224	6	ABT11088	Abt11088	Human bre
776	113	6.8	8224	7	ACC50121	Acc50121	Breast ca
777	112.5	6.8	972	4	ABA06490	Aba06490	Human cdn
778	112.5	6.8	972	6	ABV83827	Abv83827	Human pol
779	112	6.8	1190	2	AAQ51157	Aaq51157	Herpes si
780	111.5	6.7	1209	7	ACA40155	Aca40155	Prokaryot
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783	110.5	6.7	1377	3	AAQ76373	Aac76373	Human ORF
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786	109.5	6.6	1354	4	AAD08974	Aad08974	Alternati
787	109	6.6	6310	7	ACC49518	Acc49518	Tumour-as
788	108	6.5	1492	7	ABT43880	Abt43880	151P3D4 v
789	108	6.5	1492	7	ABT43881	Abt43881	DNA deriv
790	108	6.5	1640	4	AAS28787	Aas28787	Human imm
791	108	6.5	1640	4	ABA06583	Aba06583	Human cdn
792	108	6.5	1640	6	ABV83920	Abv83920	Human pol
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800	108	6.5	1957	7	ABT43866	Abt43866	DNA of tr

Search completed: August 17, 2004, 02:42:56
Job time : 504 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 16, 2004, 23:14:48 ; Search time 3044 Seconds
(without alignments)
3158.877 Million cell updates/sec

Title: US-10-063-670-6
Perfect score: 1657
Sequence: 1 MARCFSVLVLLTSIWTTRLL.....NPESKSPSKTTRVCLEAEV 322

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2 1/USPTO_spool/US10063670/runat_10082004_165353_13632/app_query.fasta_1.519
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10063670@cgn_1_1_3437@runat_10082004_165353_13632 -NCPU=6 -ICPU=3
-NO MNAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmi: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_htc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: em_gss_hum: *
18: em_gss_inv: *
19: em_gss_pln: *
20: em_gss_vrt: *
21: em_gss_fun: *
22: em_gss_mam: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rod: *
26: em_gss_phg: *
27: em_gss_vrl: *
28: gb_gss1: *

29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1657	100.0	1154	9	AL550279	AL550279 AL550279
2	1510.5	91.2	1201	9	AL550621	AL550621 AL550621
3	1480	89.3	1015	9	AL552299	AL552299 AL552299
4	1476.5	89.1	1201	9	AL546669	AL546669 AL546669
5	1439	86.8	1201	9	AL551020	AL551020 AL551020
6	1323.5	79.9	1014	9	AL553858	AL553858 AL553858
7	1316	79.4	913	13	BX459046	BX459046 BX459046
8	1283	77.4	1201	13	BX366718	BX366718 BX366718
9	1278	77.1	1172	9	AL550911	AL550911 AL550911
10	1275	76.9	972	9	AL549512	AL549512 AL549512
11	1264	76.3	911	9	AL543874	AL543874 AL543874
12	1262	76.2	1201	9	AL547774	AL547774 AL547774
13	1253	75.6	1172	9	AL552127	AL552127 AL552127
14	1243.5	75.0	1201	13	BX402505	BX402505 BX402505
15	1243	75.0	1201	9	AL544430	AL544430 AL544430
16	1235	74.5	1201	13	BX366589	BX366589 BX366589
17	1230	74.2	1116	9	AL552661	AL552661 AL552661
18	1225.5	74.0	1151	9	AL550829	AL550829 AL550829
19	1224	73.9	839	9	AL546217	AL546217 AL546217
20	1211	73.1	970	9	AL550615	AL550615 AL550615
21	1207.5	72.9	1201	9	AL546623	AL546623 AL546623
22	1168	70.5	1074	9	AL552777	AL552777 AL552777
23	1160	70.0	863	12	BI761420	BI761420 603044235
24	1142	68.9	864	9	AL545331	AL545331 AL545331
25	1103	66.6	2607	11	AK004726	AK004726 Mus muscu
26	1054.5	63.6	760	14	CB959809	CB959809 AGENCOURT
27	1019	61.5	746	14	CD238639	CD238639 FNPBCH08
28	1005.5	60.7	990	13	BX418211	BX418211 BX418211
29	970	58.5	743	9	AL598709	AL598709 DKFZp313B
30	936	56.5	1201	9	AL553712	AL553712 AL553712
31	935.5	56.5	801	12	BG483354	BG483354 602504223
32	926	55.9	794	12	BG566260	BG566260 602585128
33	922	55.6	1201	13	BX366791	BX366791 BX366791
34	905	54.6	1023	13	BY704927	BY704927 BY704927
35	901	54.4	596	9	AA046671	AA046671 zf12d09.r
36	874.5	52.8	802	14	CB994314	CB994314 AGENCOURT
37	844	50.9	1201	9	AL546565	AL546565 AL546565
38	822.5	49.6	757	14	CB229605	CB229605 AGENCOURT
39	807	48.7	877	12	BI763579	BI763579 603050140
40	795.5	48.0	964	13	BU504417	BU504417 AGENCOURT
41	766	46.2	960	9	AL553920	AL553920 AL553920
42	737	44.5	487	14	CA407758	CA407758 1003907 H
43	733.5	44.3	1298	14	CF110966	CF110966 Shultzomi
44	712.5	43.0	974	14	CB988195	CB988195 AGENCOURT
45	690	41.6	465	14	H69328	H69328 yul9a09.rl

ALIGNMENTS

RESULT 1
AL550279
LOCUS AL550279 1154 bp mRNA linear EST 31-MAY-2003
DEFINITION Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI039yJ06 5-PRIME, mRNA sequence.
ACCESSION AL550279
VERSION AL550279.2 GI:31272096
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1154)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12887098.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI039DE03QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI039DE03QP1.

FEATURES
source
1. .1154
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI039YJ06"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 9.19e-143 Length: 1154
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-063-670-6 (1-322) x AL550279 (1-1154)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 122 ATGCCAGGTCCTTCAGCCTGGTGTTCCTTCTCACTTCCATCTGGACCAAGGCTCCTG 181

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 182 GTCCAAGGCTCTTTGGTGCAGAGAGCTTTCATCCAGGTGTCTATCGAAGATTATGGG 241

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 242 ATCACCCCTGTGACAAAAGCGAACCAGCAGCTGAATTTTCACAGAGCTAAGGAGCC 301

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 302 TGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 361

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 362 AGCTTTGAAACTTCAGCTATGGCTGGTTCGAGATGGATTTCGTGGTCACTCTAGGATT 421

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 422 AGCCCAACCCCAAGTGTGGGAAAATGGGTGGGTGCTCCTGATTGTGAAGGTTCCAGTG 481

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 482 AGCCGACAGTTTGAGCCTATTGTTACAACTCATCTGATCTTGGACTAACTCGTGCAAT 541

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 542 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACCTGCAACACAACA 601

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

Db 602 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 661

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

Db 662 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT 721

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

Db 722 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 781

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

Db 782 GAAATATAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGAGGTTGCCCCACGGCTCTG 841

QY 241 LeuValLeuAlaLeuLeuphePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

Db 842 CTAGTGCTTGCTCTCCTCTCTTTTGGTGTGCTGCAGTGGTCTTGGATTTTGGTATGTCAA 901

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280

Db 902 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACC 961

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300

Db 962 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATAGGGAATCAAGAAAAACT 1021

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320

Db 1022 GATAAAAACCCAGAGAGTCCAGAGTCCAAAGAGTCCAAAGCAAAACTACCGTGCATGCGAAGCT 1081

QY 321 GluVal 322

Db 1082 GAAGTT 1087

RESULT 2
AL550621

LOCUS

DEFINITION AL550621 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI058YN14 5-PRIME, mRNA sequence.

ACCESSION AL550621

VERSION AL550621.2 GI:31272438

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12887768.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI058DG07QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI058DG07QP1.

FEATURES
source
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI058YN14"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)

primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 3.64e-129 Length: 1201
Score: 1510.50 Matches: 296
Percent Similarity: 95.53% Conservatives: 3
Best Local Similarity: 94.57% Mismatches: 11
Query Match: 91.16% Indels: 3
DB: 9 Gaps: 1

US-10-063-670-6 (1-322) x AL550621 (1-1201)

QY	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
Db	158	ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTCCATCTGGACCACGAGGCTCCTG	217
QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	218	GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTCCATCAGGTGTCATGCAGAAATATGGGG	277
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	278	ATCACCCCTGTGAGCAAAAAGCGGAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC	337
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	338	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAACAGCCTTGAAAGCT	397
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	398	AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCTGGTTCATCTTAGGATT	457
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	458	AGCCCAAACCCCAAGTGTGGAAAAAATGGGGTGGGTGCTCTGATTGGGAAGGTTCCAGTG	517
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	518	AGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGATACTTGGACTAACTCGTGCA	577
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	578	CCAGAAATTATACCCACCAAGATCCCATATTCAACACTCAAACTGCAACACACAACAACA	637
QY	161	GlupheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	638	AAATTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACTGCC	697
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	698	CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT	757
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	758	TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCAATTGTT	817
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	818	GAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGGCTCTG	877
QY	241	LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	878	CTAGTGCTTGCTCTCCTCTCTTTGGTGTGCAGCTGGTCTTGGAATTTGCTATGCAAA	937
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	938	AGGTATGTGAAGGCCCTTCCCTTTTACAAAMAARAATCAGCMGAAGGAAATGWTGADACC	997
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300

Db	998	MAAGTAGTAAAGGAGGAGCAATGATWASACCCYAATGAGGGATCAAGAAAAACT	1057
QY	301	AspLysAsnProGluSerLysSerProSerLysThr	313
Db	1058	GWTAACCCCG-----AAGAGTCCAGAGTCMAGC	1087

RESULT 3
AL552299
LOCUS
DEFINITION AL552299 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI069YN02 5-PRIME, mRNA sequence.
ACCESSION AL552299
VERSION AL552299.2 GI:31274114
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12891068.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI069DG01QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0DI069DG01QP1.

FEATURES
source
1..1015
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI069YN02"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Alignment Scores:
Pred. No.: 1.9e-126 Length: 1015
Score: 1480.00 Matches: 288
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 89.32% Indels: 0
DB: 9 Gaps: 0
US-10-063-670-6 (1-322) x AL552299 (1-1015)

QY	1	MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
Db	144	ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG	203
QY	21	ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	204	GTCCAAGGCTCTTTGCGTGCAGAGAGCTTTCATCCAGGTGTCATGCAGAAATATGGGG	263
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	264	ATCACCCCTTGTGAGCAAAAAGGGGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC	323
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80

Db 324 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 383

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||||

Db 384 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTGCTGGTCATCTCTAGGATT 443

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||||

Db 444 AGCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTGGAAGGTTCCAGTG 503

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||||

Db 504 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT 563

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||

Db 564 CCAGAAATTATCACCAAAAGATCCCATATTCCAACACTCAAACTGCAACACAACAACA 623

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
|||||

Db 624 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 683

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
|||||

Db 684 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTTATTCACGGAGAAAAAATTGATT 743

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
|||||

Db 744 TGTGTCACAGAAGTTTATTGGAACACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 803

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
|||||

Db 804 GAAATATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 863

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
|||||

Db 864 CTAGTGTCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGCTTGGATTTTGTATGTCAAA 923

QY 261 ArgTyrValLysAlaPhePropheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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Db 924 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAATGATCGAAACC 983

QY 281 LysValValLysGluGluLysAla 288
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Db 984 AAAGTAGTAAAGGAGGAGAGGCC 1007

RESULT 4

AL546669

LOCUS

DEFINITION AL546669 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI029YJ09 5-PRIME, mRNA sequence.

ACCESSION AL546669

VERSION AL546669.2 GI:31268502

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 1201)

TITLE Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

JOURNAL Full-length cDNA libraries and normalization

COMMENT Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12880008.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5952.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI029CE05QP1&cluster=5952.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

FEATURES

source

1..1201

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DI029YJ09"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.: 5.13e-126 Length: 1201

Score: 1476.50 Matches: 302

Percent Similarity: 96.24% Conservative: 5

Best Local Similarity: 94.67% Mismatches: 11

Query Match: 89.11% Indels: 5

DB: 9 Gaps: 1

US-10-063-670-6 (1-322) x AL546669 (1-1201)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
|||||

Db 126 ATGCCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 185

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||

Db 186 GTCCAAGGCTCTTTGGGTGCAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 245

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||

Db 246 ATCACCTTGTGAGCAAAAAGGGCAACCAAGCTGAATTTACAGAAAGCTAAGAGGCC 305

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||

Db 306 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGACCAAGTTGAAACAGCCTTGAAAGCT 365

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||||

Db 366 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTGCTGGTCATCTCTAGGATT 425

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||||

Db 426 AGCCCAAACCCCAAGTGTGGAAAAATGGGGTGGGTGCTCTGATTGGAAGGTTCCAGTG 485

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||||

Db 486 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT 545

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||

Db 546 CCAGAAATTATCACCAAAAGATCCCATATTCCAACACTCAAACTGCAACACAACAACA 605

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
|||||

Db 606 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 665

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
|||||

Db 666 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCCATTTCCACGGAGAAAAAATTGATT 725

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
|||||

Db 726 TGTGTCACAGAAGTTTATTGGAACACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 785

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
|||||

Db 786 GAAATATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 845

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
|||||
Db 846 CTAGTGCTTGCTCTCTCTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA 905

QY 261 ArgTyrValLysAlaPhePropheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
|||||
Db 906 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC 965

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
|||||
Db 966 ACAGTAGTAAAGGAGGR-GAGGGCAATGATAGCAM-CCTAATGRGGATC--AAAGAAACT 1021

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGlu 319
|||||
Db 1022 GATAAAA-CCAGAAGAGTCCAGA---GTCCAGCAAACTTMCGTGCGATGCTCGGAG 1074

RESULT 5
AL551020 1201 bp mRNA linear EST 31-MAY-2003
LOCUS AL551020 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI066YL13 5-PRIME, mRNA sequence.

ACCESSION AL551020
VERSION AL551020.2 GI:31272837
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12888564.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI066CF07QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI066CF07QP1.

FEATURES
source Location/Qualifiers
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI066YL13"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 1.53e-122 Length: 1201
Score: 1439.00 Matches: 300
Percent Similarity: 94.98% Conservative: 3
Best Local Similarity: 94.04% Mismatches: 14
Query Match: 86.84% Indels: 7
DB: 9 Gaps: 2

US-10-063-670-6 (1-322) x AL551020 (1-1201)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
|||||

Db 98 ATGGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCACITCCATCTGGACCACGAGGCTCCTG 157

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||
Db 158 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTTCATGCAGAAATTATGGGG 217

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||
Db 218 ATCACCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 277

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||
Db 278 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCCTGAAAGCT 337

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||||
Db 338 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCTGTGGTCTATCTTAGGATT 397

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||||
Db 398 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTCTGATTTGGAAGGTTCCAGTG 457

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||||
Db 458 AGCCGACAGTTTGCAGCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT 517

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||
Db 518 CCAGAAATTATCACCCAAAGATCCCATATTTCACACTCAAACCTGCAACACAAACAACA 577

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
|||||
Db 578 GAATTTATTGTCAGTGACAGTACCTACTCTGGTGGCATCCCCTTACTCTACAATACCTGCC 637

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
|||||
Db 638 CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTTCCACGGAGAAAAAATGATT 697

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
|||||
Db 698 TGTGTACAGAAAGTTTATGGAACCTAGCACCATGTCTACAGAACTGAACCATTTGTT 757

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
|||||
Db 758 GAAATAAAGCAGCATTCAAGAAATGAAGCTGCTGGTGTGGAGGTGTCCCCACCGCTCTG 817

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
|||||
Db 818 CTAGTGCTTGCTCTCTCTCTTCTTTGGTGTCTGCAGCTGGTCTTGGATTTTGTATGTCAAA 877

QY 261 ArgTyrValLysAlaPhePropheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
|||||
Db 878 AGGTATGTGAAGGC-TTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC 936

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
|||||
Db 937 AAGTA-GTAAAGGDCGAGAGGGC-AATGATAGCAA-CCTAATGAGGA-TCAAGAAAAACT 992

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGlu 319
|||||
Db 993 GATAAAAACC---AGAAAGAGTCAAGAGTCCAGCAAACTACGKG---CGATGCTKGCAG 1043

RESULT 6
AL553858 1014 bp mRNA linear EST 31-MAY-2003
LOCUS AL553858 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI077YL17 5-PRIME, mRNA sequence.

ACCESSION AL553858
VERSION AL553858.2 GI:31275672
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1014)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12894087.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI077CE09QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI077CE09QP1.

FEATURES
source
1. .1014
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI077YJ17"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 5.96e-112 Length: 1014
Score: 1323.50 Matches: 272
Percent Similarity: 98.55% Conservatives: 0
Best Local Similarity: 98.55% Mismatches: 4
Query Match: 79.87% Indels: 4
DB: 9 Gaps: 0

US-10-063-670-6 (1-322) x AL553858 (1-1014)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 162 ATGGCCAGGTGCTTCAGCCTGGTGTGTTCTCTCACTCCATCTGGACCACGAGGCTCCTG 221
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 222 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCTATGCAGAAATATGGGG 281
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 282 ATCACCCCTTGTGAGCAAAAAGCGAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 341
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 342 TGTAGGCTGCTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 401
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 402 AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTCGTGGTCATCTCTAGGATT 461
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 462 AGCCCAAACCCCAAGTGGGAAAAAATGGGTGGGTGGTCTCTGATTGGGAAGGTTCCAGTG 521
QY 121 SerArgGlnPheAlaIaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 522 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGACTTGGACTAATCGTGCATT 581
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 582 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 641

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 642 GAATTTATTGTCAGTACAGTACTACTCGGTGGCATCCCCTTACTCTACAAATACCTGCC 701
QY 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 702 CCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATGATT 761
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 762 TGTGTACAGAAAGTTTATTGGAACACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 821
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 822 GAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGT-CCACAGGCTCTG 880
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 881 CTAGTGCTTGCTCTCTCTTCTTTGGTGTCTGAGCTGGTCTTGGATTTTGTATGTCAA- 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGlu 276
Db 940 AGGTATGTGAAGGCTT--CCYTTTACAACAR-AATCAGCAGAGGAA 984

RESULT 7

EX459046
LOCUS BX459046 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE011YN20
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX459046
VERSION BX459046.1 GI:31021086
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE011DG10QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DE011DG10QP1.

FEATURES

source
1. .913
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE011YN20"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo (dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Alignment Scores:
Pred. No.: 2.53e-111 Length: 913
Score: 1316.00 Matches: 260
Percent Similarity: 99.62% Conservatives: 0
Best Local Similarity: 99.62% Mismatches: 1
Query Match: 79.42% Indels: 1


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DB: 13 Gaps: 0
US-10-063-670-6 (1-322) x BX459046 (1-913)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 132 ATGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCAGCTTCCATCTGGACCACGAGGCTCCTG 191
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 192 GTCCAAGGCTCTTTGGTGCAGAAAGAGCTTCCATCCAGGTGTCATGCAGAAATTATGGGG 251
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 252 ATCACCCCTTGTGAGCAAAAGCGAACACAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 311
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 312 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGACCAAGTTGAAACAGCCTTGAAAGCT 371
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 372 AGCTTTGAAACTTGCAGCTATGCCTGGTGGATGGATGGATGGTGCATCTCTAGGATT 431
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 432 AGCCCAAACCCCAAGTGTGGGAAAAATGGGTGGTGTCTGTGATTGGGAAGTTCCAGTG 491
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 492 AGCCGACAGTTTGCAGCCCTATGTTACAACCTCATCTGATACTTGGACTAACTCGTGCA 551
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 552 CCAGAAATTATCACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 611
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 612 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 671
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 672 CCTACTACTACTCTCTCTCCAGCTTCCACTTCTATTTCCACGGAGAAAAAATTGATT 731
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 732 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGCTACAGAAACTGAACCATTTGTT 791
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 792 GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGT-CCCACGGCTCTG 850
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 851 CTAGTGCTTGCTCTCCTCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAA 910
QY 261 Arg 261
Db 911 AGG 913
RESULT 8
BX366718 1201 bp mRNA linear EST 08-MAY-2003
LOCUS BX366718 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSODI040YD03 5-PRIME, mRNA sequence.
ACCESSION BX366718
VERSION BX366718.1 GI:30451557
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
```

```
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0AI040CB02QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0AI040CB02QP1.
FEATURES
Location/Qualifiers
source
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI040YD03"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
```

ORIGIN

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Alignment Scores:
Pred. No.: 4.33e-108 Length: 1201
Score: 1283.00 Matches: 260
Percent Similarity: 94.89% Conservative: 0
Best Local Similarity: 94.89% Mismatches: 14
Query Match: 77.43% Indels: 2
DB: 13 Gaps: 0
US-10-063-670-6 (1-322) x BX366718 (1-1201)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 212 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACCACGAGGCTCCTG 271
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 272 GTCCAAGGCTCTTTGGCTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 331
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 332 ATCACCCCTTGTGAGCAAAAAGCGGAACCAAGCAGCTGAATTTACAGAAGCTAAGGAGCC 391
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 392 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 451
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 452 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCACTCTTAGGATT 511
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 512 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTCTGATTTTGGAAGGTTCCAGTG 571
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 572 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCA 631
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 632 CCAGAAATTATCACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 691
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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Db 692 GAATTTATTGTCACTGACAGTAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 751

Qy 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

Db 752 CCTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT 811

Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

Db 812 TGTGTCACAGAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 871

Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

Db 872 GAAAAATAAGCAGCATTMAAGAATKAAGCTGCTGGGTTTKG-AKGTKTCCCAKGGCTCTG 930

Qy 241 LeuValLeuAlaLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260

Db 931 CTAGTGCTTKCTCTCCTCTCTTTGGTGCTGCAGCTGGTCTTGKATTTTKCTATGTCAAC 990

Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGln 274

Db 991 ADGTATGTGAAGGMCAA-CCTTTTMCACMAGAATCAGCAG 1031

RESULT 9

AL550911

LOCUS

DEFINITION

AL550911

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AL550911 1172 bp mRNA linear EST 31-MAY-2003

AL550911 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

clone CS0DI065YD17 5-PRIME, mRNA sequence.

AL550911

AL550911.2 GI:31272728

EST.

Homosapiens (human)

Homosapiens

Homosapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1172)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12888352.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5952.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI065CB09QP1&cluster=5952.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Paraday Avenue Genoscope sequence ID : CS0DI065CB09QP1.

FEATURES

Location/Qualifiers

1..1172

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DI065YD17"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.: 1.21e-107 Length: 1172

Score: 1278.00 Matches: 277

Percent Similarity: 91.29% Conservative: 6

Best Local Similarity: 89.35% Mismatches: 24

Query Match: 77.13% Indels: 9

DB: 2 Gaps: 2

US-10-063-670-6 (1-322) x AL550911 (1-1172)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

Db 154 ATGGCCAGGTGCTTCAGCCTGGTGTGTTCTTCTSACTTSCATCTGGACCACGAGGTCCTG 213

Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db 214 GTCCAAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGGTGTCTATGSAGAAATTATGGG 273

Qy 41 IleThrLeuValSerLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

Db 274 ATSAACCTTGTGAGCAAAAAGGGAASCAGCAGCTGAATTTASAGAAGCTAAGGAGGCC 333

Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

Db 334 TGTAGGCTGCTGGGACTAAGTTTGGCCGGAAGGACCAAGTTGAAACAGCCTTGAAAGCT 393

Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

Db 394 AGCTTTGAAACTTGCAGCTATGGSTGGTTGGAGATGGATTSGTGGTCATCTCTAGGATT 453

Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

Db 454 AGCSCAAACSCCAAGTGTGGAAAAAATGGGGTGGTGTCTGATTTTGGAAGGTTCCAGTG 513

Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

Db 514 AGCSGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT 573

Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

Db 574 SSAGAAATTATSAACCAAAAGATCCCATATTTCACACTCAAACGTCAACACAAACAACA 633

Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThr-IleProAl 180

Db 634 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACGAATACCTGS 693

Qy 180 aProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

Db 694 SCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGAT 753

Qy 200 eCysValThrGluValPheMetGluThrSerThrSerThrMetSerThrGluThrGluProPheVa 220

Db 754 TTGTGTSACAGAAGTTTTTATGGAACACTAGCACCATGTCTACAAAAACTGAACCATTTGT 813

Qy 220 lGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLe 240

Db 814 TGAAAAATAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGT-CCCACGGCTCT 872

Qy 240 uLeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrVally 260

Db 873 GCTAGTGCTTGCTCTCCTCTCTTTTGGTGTGCTGCAGCTGGTCTTGGATTTTGTCTATGTCAA 932

Qy 260 sArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluTh 280

Db 933 AAGGTATGTGAAGGCSSTTCCCTTTTACAAACAGRAT-CACGAGAAGGA-ATGATCGGAAC 990

Qy 280 rLysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysTh 300

Db 991 CAAGTA-GTAAAGGAGGAGAGGC--AATGATAGCAC-CCTAATGAGGAT---CAAGAAAC 1043

Qy 300 rAspLysAsnProGluGluSerLysSer 309

Db 1044 TGACAAAAAAMWC---MGAAGRTCAAARTCA 1068

RESULT 10

AL549512

LOCUS

DEFINITION

ACCESSION

VERSION

AL549512 972 bp mRNA linear EST 31-MAY-2003

AL549512 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

clone CS0DI044YN16 5-PRIME, mRNA sequence.

AL549512

AL549512.2 GI:31271330

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 972)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12885569.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI044DG08QPl&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI044DG08QPl.
Location/Qualifiers
1. .972
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI044YN16"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 1.74e-107 Length: 972
Score: 1275.00 Matches: 261
Percent Similarity: 96.36% Conservative: 4
Best Local Similarity: 94.91% Mismatches: 9
Query Match: 76.95% Indels: 4
DB: 9 Gaps: 1

US-10-063-670-6 (1-322) x AL549512 (1-972)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 143 ATGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCACTTCATCTGGACCACGAGGCTCCTG 202

QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 203 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCAATGAGG 262

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 263 ATCACCCTTGTGAGCCAAAGCGAACCAGCAGCTGAATTTACAGAAGCYAAGGAGGCC 322

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 323 TGTAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAACAGCCTTGAAGCY 382

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db 383 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCTGGGTCACTCTAGGATT 442

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 443 AGCCCAAAACCCCAAGTGTGGGAAAATGGGTGGGTGCTCCTGATTGGAAGGTTCCAGTG 502

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 503 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTGGACTAATCTCGTGCATT 562

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 563 CCAGAAATTATCACCAACAAAGATCCCATATTCAACACTCAAACCTGCAACACAAACA 622

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 623 GAATTATTGTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 682

QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 683 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 742

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 743 TGTGTSACAGAAAGTTTTTATGGAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 802

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 803 GAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTGGAGGTGTCCTCCMCG-GCTCTK 861

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 862 CTAGTGCTTKCTCTCCTCTCTTCTTGGTGTGTM-GCTGGTCTTGGATTTTGCTATGT-AAA 919

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLys 275
Db 920 AGGTATGTRAGGSCT---TCCTTTTWCAMAAGAATAASAGAAGG 961

RESULT 11
AL543874
LOCUS
DEFINITION AL543874 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI005YG13 5-PRIME, mRNA sequence.
ACCESSION AL543874
VERSION AL543874.2 GI:31265719
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 911)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12876353.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI005AD07QPl&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI005AD07QPl.
Location/Qualifiers
1. .911
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI005YG13"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source
ORIGIN
Alignment Scores:


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Pred. No.:      1.65e-106      Length:      911
Score:          1264.00      Matches:      251
Percent Similarity: 99.60%      Conservative: 0
Best Local Similarity: 99.60%      Mismatches: 1
Query Match:    76.28%      Indels:      1
DB:             9      Gaps:          0

US-10-063-670-6 (1-322) x AL543874 (1-911)

QY      1  MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
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Db      155 ATGGCCAGGTGCTTCAGCGTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 214

QY      21  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
      |||
Db      215 GTCCAAGGCTCTTTGCGTCGAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 274

QY      41  IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
      |||
Db      275 ATCACCCCTGTGAGCAAAAGCGCAACCCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 334

QY      61  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
      |||
Db      335 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 394

QY      81  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
      |||
Db      395 AGCTTTGAAACTTGCAGCTATGGCTGGTGGATGGATTGCTGGTCACTCTTAGGATT 454

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
      |||
Db      455 AGCCCAAAACCCCAAGTGTGGAAAAAATGGGTGGGTCTCTGATTGGAAGGTTCCAGTG 514

QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
      |||
Db      515 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 574

QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
      |||
Db      575 CCAGAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 634

QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
      |||
Db      635 GAATTTATTGTCAGTCAGACGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 694

QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
      |||
Db      695 CCTACTACTACTCCTCTCTCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT 754

QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
      |||
Db      755 TGTGTACAGAAGTTTTTATGGAACACTAGCACCATGTCACAGAAACTGAACCAATTGTT 814

QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
      |||
Db      815 GAAAAATAAGCAGCATTCAGAAGATGAAGCTGCTGGGTTTGGAGGTGT-CCCACGGGCTCTG 873

QY      241 LeuValLeuAlaLeuPhePheGlyAlaAlaAla 252
      |||
Db      874 CTAGTGCTTGCTCTCTCTCTCTTTTGGTGTGCAGCT 909

RESULT 12
AL547774
LOCUS
DEFINITION AL547774 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI033YD11 5-PRIME, mRNA sequence.
ACCESSION AL547774
VERSION AL547774.2 GI:31269603
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE      1 (bases 1 to 1201)
AUTHORS      Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL      Unpublished (2001)
COMMENT      On Feb 15, 2001 this sequence version replaced gi:12882152.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI033CB06QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI033CB06QP1.

FEATURES
source
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI033YD11"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
```

ORIGIN

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Alignment Scores:
Pred. No.:      3.81e-106      Length:      1201
Score:          1262.00      Matches:      262
Percent Similarity: 96.00%      Conservative: 2
Best Local Similarity: 95.27%      Mismatches: 10
Query Match:    76.16%      Indels:      5
DB:             9      Gaps:          1

US-10-063-670-6 (1-322) x AL547774 (1-1201)

QY      1  MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
      |||
Db      263 ATGGCCAGGTGCTTCAGCGTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 322

QY      21  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
      |||
Db      323 GTCCAAGGCTCTTTGCGTCGAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 382

QY      41  IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
      |||
Db      383 ATCACCCCTTGTGAGCAAAAGCGCAACCCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 442

QY      61  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
      |||
Db      443 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 502

QY      81  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
      |||
Db      503 AGCTTTGAAACTTGCAGCTATGGCTGGTGGATGGATTGCTGGTCACTCTTAGGATT 562

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
      |||
Db      563 AGCCCAAAACCCCAAGTGTGGAAAAAATGGGGTGGGTCTCTGATTGGAAGGTTCCAGTG 622

QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
      |||
Db      623 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 682

QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
      |||
Db      683 CCAGAAATTATCACCCACCAAGATCCCATATTTCACAACACTCAAACTGCAACACAAACAACA 742
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QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 743 GAAFTTATTGTCAGTGACAGTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 802

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 803 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTTCACGGAGAAAAAATTGATT 862

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 863 TGTGTACAGAAGTTTATTATGGAAGTACTAGCACCATTGCTACAGAAACTGAACCATTTGTT 922

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 923 GAAAATAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCMCG-GTCTG 981

QY 241 LeuValLeuAlaLeuLeuPheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 982 CTAGTGCTTGCTCTCCTCYTCTTGGTGCTGCRST-GGTCTTGGATT-TGCTATGTCAAA 1039

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLys 275
Db 1040 RG-TATGTGAAGSCT---CCCTTTACAAMAARAATMRCAGAAGG 1080

RESULT 13
AL552127 1172 bp mRNA linear EST 31-MAY-2003
LOCUS AL552127 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI059YA12 5-PRIME, mRNA sequence.
ACCESSION AL552127
VERSION AL552127.2 GI:31273943
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1172)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12890728.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI059BA06QPl&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI059BA06QPl.
FEATURES
source
1. .1172
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI059YA12"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Alignment Scores:
Pred. No.: 2.51e-105 Length: 1172
Score: 1253.00 Matches: 258
Percent Similarity: 95.94% Conservativeness: 2
Best Local Similarity: 95.20% Mismatches: 10
Query Match: 75.62% Indels: 4
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US-10-063-670-6 (1-322) x AL552127 (1-1172)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 242 ATGCCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACCACGAGGCTCCTG 301

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 302 GTCCAAGGCTCTTTGCTGCAGAAAGAGCTTTCCATCCAGTGTTCATGCAGAAATTATGGGG 361

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 362 ATCACCCTTGTGAGCAAAAAAGGCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGCC 421

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 422 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 481

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 482 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCTGTGTCATCTCTAGGATT 541

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 542 AGCCCCAAACCCCAAGTGTGGAAAAAATGGGGTGGGTGCTCTGATTTTGGAAGGTGCCAGTG 601

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 602 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 661

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 662 CCAGAAATTATCACCAACCAAGATCCCATATTTCACACTCAAACCTGCAACACAAACAACA 721

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 722 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGGATCCCTTACTCTACAATACCTGCC 781

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 782 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT 841

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 842 TGTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACA-TTTGTT 900

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 901 GA-AATAAAGCAGCATTCAAGAAATGAAGTGTCTGGGTTTGGAGGTGTCCCCACGGCTCTT 959

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 960 CTAGTGCTTGCTCTCTCTCTTCTTTTGGTGTGCTGCACTCGGTCTKGATTTTKC-TATGTYAAA 1018

QY 261 ArgTyrValLysAlaPheProPheThrAsnLys 271
Db 1019 RGTATTTTAAGG---CTTCCYTTTAYAAACAAA 1048

RESULT 14
BX402505 1201 bp mRNA linear EST 13-MAY-2003
LOCUS BX402505 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI045YA10 5-PRIME, mRNA sequence.
ACCESSION BX402505
VERSION BX402505.1 GI:30630733
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
```

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1A1012ZA06QPl&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1A1012ZA06QPl.
FEATURES Location/Qualifiers
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 1.97e-104 Length: 1201
Score: 1243.50 Matches: 259
Percent Similarity: 97.74% Conservative: 0
Best Local Similarity: 97.74% Mismatches: 6
Query Match: 75.05% Indels: 5
DB: 13 Gaps: 0

US-10-063-670-6 (1-322) x BX402505 (1-1201)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
|||||
Db 212 ATGGCCAGGTGCTTCAGCTGGTGTGCTTCTCATCTCCATCTGGACCACGAGGCTCCTG 271
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QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||
Db 272 GTCCAAGGCTCTTTGCTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATATGGGG 331
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QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||
Db 332 ATCACCCCTGTGAGCAAAAAGCGCAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 391
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QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||
Db 392 TGTAGGCTGCTGGGACTAAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 451
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QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
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Db 452 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTGCTGTCATCTCTAGGATT 511
|||||

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||||
Db 572 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGACTTGGACTAACTCGTGCAAT 631
|||||

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||
Db 632 CCAGAAATTATCACCCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 691
|||||

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
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Db 752 CCTACTACTCTCCTCTCCAGCTTCCACTTCCACTTCTATTCCACGAGAAAAAATGATT 811
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QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
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Db 812 TGTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 871
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QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
|||||

Db 872 GAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTTGGAGGTGT-CCCACGGCTCTG 930
|||||

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
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QY 261 ArgTyrValLysAla 265
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Db 988 AG-TATGTGAAGGCT 1001
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RESULT 15
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LOCUS AL544430 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI018YG12 5-PRIME, mRNA sequence.
ACCESSION AL544430
VERSION AL544430.2 GI:31266274
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12876910.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI018BD06QPl&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI018BD06QPl.
FEATURES Location/Qualifiers
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/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 2.2e-104 Length: 1201
Score: 1243.00 Matches: 256
Percent Similarity: 95.90% Conservative: 1
Best Local Similarity: 95.52% Mismatches: 9
Query Match: 75.02% Indels: 5
DB: 9 Gaps: 2

US-10-063-670-6 (1-322) x AL544430 (1-1201)

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Db	299	GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTCCATCCAGGTGTCAATGCAGAAATTATGGGG	358
QY	41	IleThrLeuValSerLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	359	ATCACCCCTTGTAGCAAAAAGCGAACCCAGAGCTGAATTTACAGAGTAAGGAGGCC	418
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	419	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACACAGCCTTGAAAGCT	478
QY	81	SerPheGluThrCysSerTyrGlyTrrValGlyAspGlyPheValValIleSerArgIle	100
Db	479	AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTCATCTCTAGGATT	538
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrLysValProVal	120
Db	539	AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGATTTGGAAGGTTCCAGTG	598
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrrPThrAsnSerCysIle	140
Db	599	AGCCGACAGTTTGCAGCCCTATTGTTACAACTCATCTGATACCTGGACTAACTCGTGCATT	658
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	659	CCAGAAATTTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCACACAACAACA	718
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	719	GAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC	778
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	779	CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT	838
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	839	TGTGTCACAGAGTTTATTGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	898
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	899	GAAATAAAGCAGCATTCAGAATGAAGCTGTGGGTTTGGAGGTGT-CCCACGGCTCTG	957
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	958	CTAGTGCTTGCTCT-CTCTTCTTTGGTGCKSAGYGGTCT---TGGATTTGCTATGTCAA-	1012
QY	261	ArgTyrValLysAlaPheProPhe	268
Db	1013	AGGTATGTRAGGCTT---CCCTTT	1033

Search completed: August 17, 2004, 01:23:10
Job time : 3054 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2004, 01:24:53 ; Search time 538 Seconds
(without alignments)
2936.669 Million cell updates/sec

Title: US-10-063-670-6
Perfect score: 1657
Sequence: 1 MARCFSLVLLTSIWTRLL.....NPESKSPSKTTVRCLEAEV 322

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3225727 seqs, 2453303834 residues
Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 800 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO spool/US10063670/runat_10082004_165530_14795/app_query.fasta_1.519
-DB=Published Applications NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=800 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=0 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10063670@cgn_1_1_480@runat_10082004_165530_14795
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Job time : 553 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 16, 2004, 23:31:04 ; Search time 91 Seconds
(without alignments)
1963.672 Million cell updates/sec

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Perfect score: 1657
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Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues 1365418
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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1	1657	100.0	2029	4	US-09-232-160-13 Sequence 13, Appl
2	1657	100.0	2372	4	US-09-907-794A-200 Sequence 200, App
3	1657	100.0	2372	4	US-09-905-125A-200 Sequence 200, App
4	1657	100.0	2372	4	US-09-902-775A-200 Sequence 200, App
5	1657	100.0	2404	4	US-09-833-381-849 Sequence 849, App
6	1657	100.0	2404	4	US-09-833-381-853 Sequence 853, App
7	1651	99.6	2313	2	US-08-892-880-1 Sequence 1, Appli
8	1103	66.6	1896	4	US-09-724-864-28 Sequence 28, Appl
9	354	21.4	492	2	US-08-892-880-12 Sequence 12, Appl
10	349	21.1	466	2	US-08-892-880-13 Sequence 13, Appl
11	286.5	17.3	498	2	US-08-892-880-15 Sequence 15, Appl
12	234.5	14.2	1537	6	5504194-1 Patent No. 5504194

13	224	13.5	3207	1	US-07-946-497-1	Sequence 1, Appli
14	224	13.5	3207	1	US-08-483-322-1	Sequence 1, Appli
15	224	13.5	3207	2	US-08-478-882-1	Sequence 1, Appli
16	213	12.9	1794	3	US-09-213-719-1	Sequence 1, Appli
17	210	12.7	1297	4	US-09-023-655-876	Sequence 876, App
18	199.5	12.0	4675	4	US-09-566-921-97	Sequence 97, Appl
19	145	8.8	1414	1	US-08-024-868-1	Sequence 1, Appli
20	145	8.8	1414	2	US-08-242-097-1	Sequence 1, Appli
21	145	8.8	1414	3	US-09-206-695-1	Sequence 1, Appli
22	145	8.8	1414	4	US-09-799-118-1	Sequence 1, Appli
23	133.5	8.1	1734	4	US-09-484-9708-63	Sequence 63, Appl
24	128.5	7.8	3259	5	PCT-US95-03747-1	Sequence 1, Appli
25	127.5	7.7	1985	4	US-09-907-794A-212	Sequence 212, App
26	127.5	7.7	1985	4	US-09-905-125A-212	Sequence 212, App
27	127.5	7.7	1985	4	US-09-902-775A-212	Sequence 212, App
28	121	7.3	1587	4	US-09-010-147B-19	Sequence 19, Appl
29	114.5	6.9	5191	1	US-08-340-428B-1	Sequence 1, Appli
30	114.5	6.9	5191	5	PCT-US93-07306-1	Sequence 1, Appli
31	113	6.8	8224	6	5180808-1	Patent No. 5180808
32	112	6.8	1190	1	US-08-310-370-1	Sequence 1, Appli
33	111	6.7	1720	4	US-09-148-545-53	Sequence 53, Appl
34	107	6.5	1400	2	US-08-001-078A-2	Sequence 2, Appli
35	107	6.5	1400	2	US-08-463-218-2	Sequence 2, Appli
36	107	6.5	1400	5	PCT-US94-00253-2	Sequence 2, Appli
37	107	6.5	1520	1	US-08-225-477B-1	Sequence 1, Appli
38	107	6.5	1520	5	PCT-US95-04353-1	Sequence 1, Appli
39	107	6.5	2589	1	US-08-325-267A-3	Sequence 3, Appli
40	107	6.5	2685	3	US-08-362-525-21	Sequence 21, Appl
41	107	6.5	4614	1	US-08-325-267A-1	Sequence 1, Appli
42	106.5	6.4	1482	4	US-09-016-434-230	Sequence 230, App
43	106.5	6.4	2455	3	US-09-103-429A-1	Sequence 1, Appli
44	106.5	6.4	2821	3	US-09-103-429A-2	Sequence 2, Appli
45	103	6.2	1519	1	US-08-225-477B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-232-160-13
; Sequence 13, Application US/09232160
; Patent No. 6368794
; GENERAL INFORMATION:
; APPLICANT: Steve Daniel
; APPLICANT: James Gilmore
; APPLICANT: Susan G. Stuart
; APPLICANT: Laura Stuve
; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: PA-0003 US
; CURRENT APPLICATION NUMBER: US/09/232,160
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PERL program
; SEQ ID NO 13
; LENGTH: 2029
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 3044710
US-09-232-160-13

Alignment Scores:
Pred. No.: 4.6e-177 Length: 2029
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-063-670-6 (1-322) x US-09-232-160-13 (1-2029)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20
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Db 183 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCCTCATTCCATCTGGACACGAGGCTCCTG 242

Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db 243 GTCCAAGGCTCTTTCGCTGCAGAAAGCTTTCATCCAGGTGTATGCAGAAATATGGGG 302

Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

Db 303 ATCACCCCTTGTGAGCAAAAGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGCC 362

Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

Db 363 TGTAGGCTGCTGGACTAAGTTTGGCCGCAAGCAAGTTGAAACAGCCTTGAAAGCT 422

Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

Db 423 AGCTTTGAAACTTGCAGCTATGGCTGGTGGATGGATTCTGGTCACTCTTAGGATT 482

Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

Db 483 AGCCCAAACCCCAAGTGTGGGAAAAATGGGTGGTGTCTGATTGGAAGTTCCAGTG 542

Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

Db 543 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATCTTGGACTAATCGTGCAAT 602

Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

Db 603 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACCAACAACA 662

Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

Db 663 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACATACTGCC 722

Qy 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

Db 723 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT 782

Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

Db 783 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 842

Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

Db 843 GAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGTGTGGAGGTGTCCCCACGGCTCTG 902

Qy 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

Db 903 CTAGTGCTTGCTCTCTCTTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAA 962

Qy 261 ArgTyrValLysAlaPhePropheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280

Db 963 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAATGATCGAAACC 1022

Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300

Db 1023 AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACT 1082

Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320

Db 1083 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTCGATGCGCTGGAAGCT 1142

Qy 321 GluVal 322

Db 1143 GAAGTT 1148

RESULT 2

US-09-907-794A-200
; Sequence 200, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi

Alignment Scores:

Pred. No.: 5,92e-177 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0

; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-794A-200

Best Local Similarity: 100.00%		Mismatches:	0
Query Match: 100.00%		Indels:	0
DB: 4		Gaps:	0
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Db	160	ATGGCCAGGTGCTTCAGCCTGGTGTTCCTTCATCTCCATCTGGACCACGAGGCTCCTG	219
QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCAAGGCTCTTTCGGTGCAGAAAGAGCTTTCATCCAGGTGTCAATGAGAATTATGGGG	279
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCCCTTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCC	339
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTrrPValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCGTGGTCATCTCTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrPlysValProVal	120
Db	460	AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTGGAAAGGTTCCAGTG	519
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrrPThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCAAT	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA	639
QY	161	GluPheIleValSerAspSerThrTrrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATTGTCAGTGACAGTACCTACTCGTGGCATCCCTTTACTCTACAATACCTGCC	699
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGGAGAAAAAATTGATT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGCTTGCTCTCTCTCTTCTTTGTTGCTGCAGCTGGTCTTGGAATTTGCTATGTCAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGCCTTCCCTTTTACAACAAGAATCAGCAGAAGGAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr	300
Db	1000	AAAGTAGTAAGGAGGAGAGGCCAATGATAGCAACCTTAATGAGGAATCAAGAAAACT	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCTGGAAGCT	1119
QY	321	GluVal 322	
Db	1120	GAAGTT 1125	

RESULT 3
US-09-905-125A-200
; Sequence 200, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-125A-200

Alignment Scores:
Pred. No.:      5.92e-177      Length:      2372
Score:          1657.00        Matches:      322
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:      100.00%      Indels:        0
DB:              4            Gaps:          0

US-10-063-670-6 (1-322) x US-09-905-125A-200 (1-2372)

QY      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
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QY      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCCAAGGCTCTTTGCGTGCAGAAAGCTTTCATCCAGGTGTCTATGCAGAAATTATGGGG 279

QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPhetheThrGluAlaLysGluAla 60
Db      280 ATCACCCCTTGCAGCAAAAGGCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCC 339

QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      400 AGCTTTGAAACTGTCAGCTATGGCTGGGTGGAGATGGATTCGTGGTCACTCTTAGGATT 459

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      460 AGCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTGGAGGTTCCAGTG 519

QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATCTTGGACTAACTCGTGCAAT 579

QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580 CCAGAAATTTATCACCAACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACA 639

QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699

QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY      201 CysValThrGluValPheMetGluThrThrSerThrMetSerThrGluThrGluPropheVal 220
Db      760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820 GAAAATAAAGCAGCATTTCAAGAATGAAGCTGTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880 CTAGTGCTTGCTCTCTCTTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGTATGTCAA 939

QY      261 ArgTyrValLysAlaPhePropheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGATCAGCAGAGGAATGATCGAAACC 999

QY      281 LysValValLysGluGluLysAlaAsnAspSerSerProAsnGluGluSerLysLysThr 300
Db      1000 AAAGTAGTAAAGGAGAGAGGCCCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT 1059
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QY      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1060 GATAAAACCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTGGATGCTGGAAGCT 1119

QY      321 GluVal 322
Db      1120 GAAGTT 1125

RESULT 4
US-09-902-775A-200
; Sequence 200, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-775A-200

Alignment Scores:
Pred. No.:      5.92e-177      Length:      2372
Score:          1657.00        Matches:     322
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:               4           Gaps:          0

US-10-063-670-6 (1-322) x US-09-902-775A-200 (1-2372)

QY      1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219

QY      21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCCAAGGCTCTTTGGGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279

QY      41 IleThrLeuValSerLysAlaAsnGlnGlnLeuAsnPhetheThrGluAlaLysGluAla 60
Db      280 ATCACCCCTTGTGAGCAAAAAGCGAACAGCAGCTGAATTTTCACAGAACTAAGGAGGCC 339

QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGCAAGCTTGAACAGCCTTGAAGACT 399

QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGATTTCGTGTCATCTTAGGATT 459

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      460 AGCCCAAAACCCCAAGTGTGGGAAAATGGGGTGGTCTCTGATTTTGGAGGTTCCAGTG 519

QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACCTTGGACTAACTCGTGCAAT 579

QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580 CCAGAAATTTATCACCAACCAAGATCCCATATTCAAACACTCAAACTGCAACACAAACAACA 639

QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTTATTGTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTTACTCTACAATACCTGCC 699

QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      760 TGTGTACACAGAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db      820 GAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCACGGCTCTG 879

QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880 CTAGTGTCTTCTCTCTCTCTTTTGGTGTCTGCAGCTGGTCTTGGATTTTGCTATGTCAA 939
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QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAACC 999

QY      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1000 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAAC 1059

QY      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCCTGGAAGCT 1119

QY      321 GluVal 322
Db      1120 GAAGTT 1125

RESULT 5
US-09-833-381-849
; Sequence 849, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 849
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-849

Alignment Scores:
Pred. No.:      6.05e-177      Length:      2404
Score:          1657.00        Matches:     322
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:               4           Gaps:          0

US-10-063-670-6 (1-322) x US-09-833-381-849 (1-2404)

QY      1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      190 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 249

QY      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      250 GTCCAAGGCTCTTTGGGTGCAGAAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGG 309

QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPhetheThrGluAlaLysGluAla 60
Db      310 ATCACCCCTTGTGAGCAAAAAGCGAACCAAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 369

QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      370 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 429

QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      430 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGTCATCTCTAGGATT 489

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      490 AGCCCAAAACCCCAAGTGTGGGAAAATGGGGTGGGTGTCTCTGATTGGAAGGTTCCAGTG 549

QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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Db 550 AGCCGACAGTTTGAGCCTATTGTTACAACATCATCTGATCTTGGACTAACTCGTGCATT 609
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 610 CCAGAAATTATCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAACA 669
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 670 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 729
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200
Db 730 CCTACTACTACT 789
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 790 TGTGTACAGAGAGTTTATGGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 849
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 850 GAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 909
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaGlyPheGlyLeuGlyPheCysTyrValLys 260
Db 910 CTAGTGCTTGCT 969
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 970 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAATGATCGAAACC 1029
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr 300
Db 1030 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACT 1089
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1090 GATAAAACCCAGAGAGTCCAGAGTCCAGCAAAACTACCGTGCATGCGTGAAGCT 1149
QY 321 GluVal 322
Db 1150 GAAGTT 1155

RESULT 6

US-09-833-381-853
; Sequence 853, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 853
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-853

Alignment Scores:
Pred. No.: 6.05e-177 Length: 2404
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-063-670-6 (1-322) x US-09-833-381-853 (1-2404)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

Db 190 ATGCCCAGGTGCTTCAGCCTGGTGTGTTCTTCACTTCATCTGGACCAGGCTCCTG 249
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 250 GTCCAAAGGCTCTTTGGTGCAGAGAGCTTTCATCCAGGTGTCTATGAGAATTATGGG 309
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 310 ATCACCTTGTGAGCAAAAAGGGCAACAGCAGCTGAATTTACAGAACTAAGGAGGCC 369
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 370 TGTAGGCTGCTGGACTAAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 429
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db 430 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT 489
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 490 AGCCCAAAACCCCAAGTGTGGAAAAATGGGTGGGTGTCTCTGATTTGGAAGGTTCCAGTG 549
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 550 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAATCGTGCATT 609
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 610 CCAGAAATTAACACCACCAAGATCCCATATTTCAACACTCAAACCTCAAACACAACA 669
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 670 GAATTTATTGTCAGTGACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTGCC 729
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200
Db 730 CCTACTACTACT 789
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 790 TGTGTACAGAGAGTTTATGGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 849
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 850 GAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 909
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 910 CTAGTGCTTGCT 969
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 970 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAATGATCGAAACC 1029
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr 300
Db 1030 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACT 1089
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1090 GATAAAACCCAGAGAGTCCAGAGTCCAGCAAAACTACCGTGCATGCGTGAAGCT 1149
QY 321 GluVal 322
Db 1150 GAAGTT 1155

RESULT 7

US-08-892-880-1
; Sequence 1, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN

APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK J.
TITLE OF INVENTION: CD44-LIKE PROTEIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FILING DATE: HERewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,762
FILING DATE: 15-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0490001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2313 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 91..1056
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 154..1056
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 91..153
US-08-892-880-1

Alignment Scores:
Pred. No.: 2,71e-176 Length: 2313
Score: 1651.00 Matches: 321
Percent Similarity: 99.69% Conservative: 0
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 99.64% Indels: 0
DB: 2 Gaps: 0
US-10-063-670-6 (1-322) x US-08-892-880-1 (1-2313)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrrPrrThrArgLeuLeu 20
Db 91 ATGGCCAGGTCTTCAGCCTGGTGTTCCTCCTCCATCTGGACACGAGGCTCCTG 150
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 151 GTCCAAGGCTCTTGGCTGCAGAAAGAGCTTCCATCCAGGTGTCTAGCAGAAATTATGGGG 210
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 211 ATCACCCCTTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTACAGAGCTAAGGAGGCC 270
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 271 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 330

QY 81 SerPheGluThrCysSerTyrGlyTrrPrrValGlyAspGlyPheValValIleSerArgIle 100
Db 331 AGCTTTGCAACTTGCACTATGGCTGGTGGTGGATTCGTGGTCTCTAGGATT 390
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrPrrLysValProVal 120
Db 391 AGCCCAAAACCCCAAGTGTGGAAAAAATGGGGTGGTGTCTGATTTGGAGGTTCAGTG 450
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrrPrrThrAsnSerCysIle 140
Db 451 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAATCGTGCAAT 510
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 511 CCAGAAATTATCACCAACCAAGATCCCATATTAACACTCAAACTGCAACACAAACAACA 570
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 571 GAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 630
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 631 CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTTCCACGGAGAAAAAATTGATT 690
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 691 TGTGTACAGAAAGTTTATGGAACTAGACCATGTCTACAGAACTGAACCATTTGTT 750
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 751 GAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 810
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 811 CTAGTGTGCTCTCTCTCTTCTTGGTGTGCTGAGCTGGTCTTGGATTTTGTATGTCAA 870
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 871 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACC 930
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 931 AAAGTAGTAAAGGAGGAGAGGCAATGATAGCAACCCCTAATGAGGATCAAGAAAAACT 990
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 991 GATAAAACCCAGAGAGTCCAGAGTCCAGAGTCCAGCAAAACTACCGTGGATGCTGGAGCT 1050
QY 321 GluVal 322
Db 1051 GAAGTT 1056
RESULT. 8
US-09-724-864-28
; Sequence 28, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1896
; TYPE: DNA
; ORGANISM: Mouse

US-09-724-864-28				
Alignment Scores:				
Pred. No.:	1.62e-114	Length:	1896	
Score:	1103.00	Matches:	221	
Percent Similarity:	79.18%	Conservative:	30	
Best Local Similarity:	69.72%	Mismatches:	62	
Query Match:	66.57%	Indels:	4	
DB:	4	Gaps:	3	
US-10-063-670-6 (1-322) x US-09-724-864-28 (1-1896)				
QY	6	SerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeuValGlnGlySerLeu	25	
Db	77	AGCCTGGTGTTACTCCTCGCCTCTATTGGACCCTAGGCACCCAGTCCAAGGTGCCGAC	136	
QY	26	ArgAlaGluLeuSerIleGlnValSerCysArgIleMetGlyIleThrLeuValSer	45	
Db	137	CTCGTGCAAGACCTTTCATTCTCT--ACATGCAGAAATCATGGCGGTGCCCTTGTGGGC	193	
QY	46	LysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAlaCysArgLeuLeuGly	65	
Db	194	AGAAACAAAAACCCACAGATGAATTTACAGAAGCCAACGAGGCCGTGAAGATGCTGGGA	253	
QY	66	LeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAlaSerPheGluThrCys	85	
Db	254	CTGACTCTGGCCAGCAGGACCAGGTAGAGTCAGCGCAGAAATCTGGCTTTGAGACTTGC	313	
QY	86	SerTyrGlyTrpValGlyAspGlyPheValIleSerArgIleSerProAsnProLys	105	
Db	314	AGCTATGGATGGGTGGAGAACAGTTCTCTGTCATCCCTCGGATTTCTCAACCCCGAGG	373	
QY	106	CysGlyLysAsnGlyValGlyValLeuIleTrpLysValProValSerArgGlnPheAla	125	
Db	374	TGTGGGAAGAATGGCAAAAGGTGTCTGTGATTGGAAATGCTCCCTCCAGCCAAAAGTTCAAA	433	
QY	126	AlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIleProGluIleIleThr	145	
Db	434	GCCTATTGCCACAACACTCATCCGACACCTGGGTTAACTCCTGCATTCAGAAATCGTTACC	493	
QY	146	ThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThrGluPheIleValSer	165	
Db	494	ACATTTTACCCCGTGTGGACACTCAA-----ACACCCGCAACAGAGTTTCTGTCTCAGC	547	
QY	166	AspSerThrTyrSerValAlaSerProTyrSerThrIleProAlaProThrThrThrPro	185	
Db	548	AGCAGCGCCTACTTGGCTTCATCCCTGACTCCACAACACCTGTTTCTGCCACCACCC---	604	
QY	186	ProAlaProAlaSerThrSerIleProArgArgLysLysLeuIleCysValThrGluVal	205	
Db	605	CGGGCTCCACCTTTGACCTCCATGGCACGGAACACAAAAGATTTGTATCAGGAAGTT	664	
QY	206	PheMetGluThrSerThrMetSerThrGluThrGluProPheValGluAsnLysAlaAla	225	
Db	665	TATACAGAACCTATCACCATGGCTACAGAAACAGAACGATTTGTTGCAAGTGGAGCAGCA	724	
QY	226	PheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeuLeuValLeuAlaLeu	245	
Db	725	TTCAAGAACGAAGCAGCTGGGTTTGAGGTGTCCCCACCGCCCTGTGTGGTGGCTCTC	784	
QY	246	LeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLysArgTyrValLysAla	265	
Db	785	CTCTTCTTTGGTGTGCCGCTGTGCTGGCTGTTGTGTACGTGAAAGGTATGTGAAGGCC	844	
QY	266	PheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThrLysValLysGlu	285	
Db	845	TTCCCTTTCAACCAAGAATCAACAGAAGGAATGATCGAAACCAAGTTGTAAAGGAA	904	
QY	286	GluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThrAspLysAsnProGlu	305	
Db	905	GAGAAGGCTGATGACGTCAACGCTAATGAAGAATCAAAGAAACCATTTAAACCCAGAG	964	
QY	306	GluSerLysSerProSerLysThrThrValArgCysLeuGluAlaGluVal	322	

Db	965	GAGGCCAAGAGTCCACCCAAACTACGGTGGATGCTTAGAAGCTGAAGTT	1015	
RESULT 9				
US-08-892-880-12				
; Sequence 12, Application US/08892880				
; Patent No. 5942417				
; GENERAL INFORMATION:				
; APPLICANT: NI, JIAN				
; APPLICANT: GENTZ, REINER L.				
; APPLICANT: DILLON, PATRICK J.				
; TITLE OF INVENTION: CD44-LIKE PROTEIN				
; NUMBER OF SEQUENCES: 15				
; CORRESPONDENCE ADDRESS:				
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.				
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600				
; CITY: WASHINGTON				
; STATE: DC				
; COUNTRY: USA				
; ZIP: 20005-3934				
; COMPUTER READABLE FORM:				
; MEDIUM TYPE: Floppy disk				
; COMPUTER: IBM PC compatible				
; OPERATING SYSTEM: PC-DOS/MS-DOS				
; SOFTWARE: PatentIn Release #1.0, Version #1.30				
; CURRENT APPLICATION DATA:				
; APPLICATION NUMBER: US/08/892,880				
; FILING DATE: HERewith				
; CLASSIFICATION: 435				
; PRIOR APPLICATION DATA:				
; APPLICATION NUMBER: 60/021,762				
; FILING DATE: 15-JUL-1996				
; ATTORNEY/AGENT INFORMATION:				
; NAME: STEFFE, ERIC K				
; REGISTRATION NUMBER: 36,688				
; REFERENCE/DOCKET NUMBER: 1488.0490001				
; TELECOMMUNICATION INFORMATION:				
; TELEPHONE: 202-371-2600				
; TELEFAX: 202-371-2540				
; INFORMATION FOR SEQ ID NO: 12:				
; SEQUENCE CHARACTERISTICS:				
; LENGTH: 492 base pairs				
; TYPE: nucleic acid				
; STRANDEDNESS: single				
; TOPOLOGY: linear				
; MOLECULE TYPE: cDNA				
US-08-892-880-12				
Alignment Scores:				
Pred. No.:	7.76e-31	Length:	492	
Score:	354.00	Matches:	83	
Percent Similarity:	77.39%	Conservative:	6	
Best Local Similarity:	72.17%	Mismatches:	12	
Query Match:	21.36%	Indels:	16	
DB:	2	Gaps:	2	

US-10-063-670-6 (1-322) x US-08-892-880-12 (1-492)				
QY	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu	20	
Db	99	ATGCCAGGTGCTTCAGCCTGGTGTGTTGCTTNTCACTTCATCTGGACCACGAGGCTCCTG	158	
QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40	
Db	159	GTCCAAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG	218	
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60	
Db	219	ATCACCCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGC	278	
QY	61	CysArgLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80	
Db	279	TGTAGTTGCTNGGACTAAGTTTGGCCGCGCAAGGCCAGTTG---AACAGCTTGAAGT-	334	

QY 81 SerPheGluThrCysSerTyrGlyTrpValGly----- 91
Db 335 AGCTTTGAAT-TGCAGTTTGGCTTGGTTGGATGGTTTCGNGNCATTTAGTTAGTCCCAA 393
QY 92 -----AspGlyPheValValIleSerArgIleSerPro 102
Db 394 CCCANTTTGGAAANTGGGTGNNCNATTTGNAGTCCCTTAGCCCN 438
RESULT 10
US-08-892-880-13
; Sequence 13, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HERewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-892-880-13

Alignment Scores:
Pred. No.: 2.61e-30 Length: 466
Score: 349.00 Matches: 89
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 82.41% Mismatches: 10
Query Match: 21.06% Indels: 8
DB: 2 Gaps: 2

US-10-063-670-6 (1-322) x US-08-892-880-13 (1-466)

QY 219 PheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThr 238
Db 15 TTTGTTGAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACG 74
QY 239 AlaLeuLeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCystYr 258
Db 75 GCTCTGCTAGTGTGCT 134
QY 259 ValLysArgTyrVal-LysAlaPheProPheThrAsnLysAsnGlnGlnLys-GluMetI 278

Db 135 GTCAAAAGGTATGTGAAAGGCCTTCCCTTTTACAAACAAGAATCNGCAGAGGGAATGA 194
QY 278 leGluThrLysValVal-LysGluGluLysAlaAsnAspSerAsnPro-AsnGluGluse 297
Db 195 TCGAAACCAAGTAGTGAAGGAGGAGAGCAATGNTAGCAACCTGAATGAGGATT 254
QY 297 rLys--LysThrAspLysAsnPro---GluGluSerLysSerProSerLysThr-ThrV 315
Db 255 CAAAGGAAACTGNTTAAAAACCCAGTAGNAGTTCAGAGAGTNCACCAAGCAAACTTACCG 314
QY 315 al-ArgCysLeu 318
Db 315 TGTCGATGCCTG 326
RESULT 11
US-08-892-880-15
; Sequence 15, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HERewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-892-880-15

Alignment Scores:
Pred. No.: 3.35e-23 Length: 498
Score: 286.50 Matches: 62
Percent Similarity: 90.00% Conservative: 1
Best Local Similarity: 88.57% Mismatches: 4
Query Match: 17.29% Indels: 3
DB: 2 Gaps: 1

US-10-063-670-6 (1-322) x US-08-892-880-15 (1-498)

QY 254 LeuGlyPheCysTyrValLysArgTyrValLysAlaPheProPheThrAsnLysAsnGln 273
Db 14 CTGGATTTTGCTATGTCAAAAGGTATGTNAAGGCCTTCCCTTTTACAAACAAGATCAG 73


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.; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: p-Meta-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 113..1624
US-08-483-322-1

Alignment Scores:
Pred. No.: 7.8e-15 Length: 3207
Score: 224.00 Matches: 87
Percent Similarity: 37.68% Conservative: 43
Best Local Similarity: 25.22% Mismatches: 171
Query Match: 13.52% Indels: 44
DB: 1 Gaps: 12

US-10-063-670-6 (1-322) x US-08-483-322-1 (1-3207)

QY 3 ArgCysPheSerLeuValLeuLeuLeuThr-----SerIleTrpThr 16
Db 86 AGATCCTTTGGTTTCATCCTGCACATCATGGACAAGGTTTGGTGGCACACAGCTTGGGGA 145

QY 17 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 36
Db 146 CTACTTTGCCTCTTACAGTTTGAGCCTGGCACAGCAGCAGATCGATTTGAATATAACCTGC 205

QY 37 ArgIleMetGlyIleThrLeuValSerLeuSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 56
Db 206 CGTTACGCAGGTGTTATTCATGTGGAGAAAATGGCCGCTACAGTATCTCCAGGACTGAA 265

QY 57 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 76
Db 266 GCAGCTGACCTCTGCGAGGCTTTCAACACCACCTTGCCCACTGGCTCAGATGGAGTTA 325

QY 77 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 96
Db 326 GCCCTGAGAAAGGGTTTGAACATGCAGGTATGGGTTTCATA--GAAGGACACGTGGTA 382

QY 97 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 116
Db 383 ATCCCGAGGATCCACCCCAACGCTATCTGTGCAGCAACCAACACACAGGAGTGTATATCCTC 442

QY 117 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 136
Db 443 CTCGCATCCAACACCTCCCACTATGACACATATGCTTCAATGCCTCAGCTCCTCTTGAA 502

QY 137 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 156
Db 503 GAAGACTGT-----ACATCAGTCACAGACCTACCCAATTCCTTCGATGGA 547

QY 157 ThrGlnThrThrGluPheIleValSerAspSerThr---TyrSerValAlaSerProTyr 175
Db 548 CCAGTTACCATAACTATTGTCAACCGTGATGGCACCCGCTACAGCAAGAGGGCGAGTAT 607

QY 176 SerThr-----IleProAlaProThr----- 182
Db 608 AGAACACACCAAGAGACATCGATGCCTCAAAATATATAGATGAGGATGTCAGCAGTGGA 667

QY 183 -----ThrThrProProAla---ProAlaSerThrSerIleProArgArg 196
Db 668 TCCACCATTTGAGAAGAGACCCCAAGGCTACATTTTGCACACCGACCTTCCCACTTCA 727

QY 197 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThr---Glu 215
Db 728 CAGCCTACTGGAGACCGGGATGACGCCTTCTTTATTGGGAGCACCTGGCCCACTTGA 787

QY 216 ThrGluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGly 235
Db 788 ACTACTCCATGGGTTTCTGCCCCACACAAACAGAACAGGACCGCCAGTGGAAACCCG 847

QY 236 Val-----ProThrAlaLeuLeuValLeuAlaLeuLeuPhePheGlyAlaAlaAla 252
Db 848 ATCCATTCAAACCCAGAAAGTACTACTTCAGACAAACCACCAAGGATGACTGATATAGACAGA 907
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QY 253 GlyLeuGlyPheCysTyrValLysArgTyrValLys-----AlaPheProPheThrAsn 270
Db 908 AACAGCACCATGCTCATGGAGAAAACCTGGACCCAGGAACACAGCCTCTTCAATAAC 967

QY 271 LysAsnGlnGlnLysGluMetIleGluThrLysValLysGluGluLysAlaAsnAsp 290
Db 968 CATGAGTATCAGCATGAAGAG--GAGACCCCATGTCTACAAGCACACCTGGGCAGAT 1024

QY 291 SerAsnProAsnGluGluSerLysLysThrAspLys-----AsnProGlu 305
Db 1025 CCTAATAGCAACAACAGAGAAGCAGCTACCCAGAAGGAGAAGTGGTTTGAGAAATGAATGG 1084

QY 306 GluSerLysSerPro 310
Db 1085 CAGGGGAAGAACCCA 1099

RESULT 15
US-08-478-882-1
; Sequence 1, Application US/08478882
; Patent No. 5885575
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHERT, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,882
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,497
; FILING DATE: 19921109
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: p-Meta-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 113..1624
US-08-478-882-1

Alignment Scores: 7.8e-15 Length: 3207
Pred. No.: 224.00 Matches: 87
Score: 224.00
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Percent Similarity: 37.68%
Best Local Similarity: 25.22%
Query Match: 13.52%
DB: 2

Conservative: 43
Mismatches: 171
Indels: 44
Gaps: 12

US-10-063-670-6 (1-322) x US-08-478-882-1 (1-3207)

QY 3 ArgCysPheSerLeuValLeuLeuLeuThr-----SerIleTirpThr 16
||| ||| ::||| :::
Db 86 AGATCCTTTGGTTTCATCCTGCACATCATGGACAAGTTTGGTGGCACACAGCTTGGGA 145

QY 17 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 36
|||::||| ||||| ::::: :::
Db 146 CTACTTTGCCCTCTACAGTTGAGCCTGGCACACAGCAGATCGATTTGAATATAACCTGC 205

QY 37 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 56
|||::||| ||| ||| ::::: |||||
Db 206 CGTTACGCAGGTGTATTCCATGTGGAGAAAATGGCCGCTACAGTATCTCCAGGACTGAA 265

QY 57 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 76
|||::||| ::||| ::::: |||||
Db 266 GCAGCTGACCTCTGCGAGGCTTTCAACACCCACCTTGCCACCATGGCTCAGATGGAGTTA 325

QY 77 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTirpValGlyAspGlyPheValVal 96
|||::||| ||||| ||||| ::::: |||||
Db 326 GCCCTGAGAAAGGGTTTGAAACATGCAGGTATGGGTTTATA--GAAGGACACGTGGTA 382

QY 97 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValIleIleTirp 116
|||::||| ||||| ||||| |||||
Db 383 ATCCCGAGGATCCACCCCAACGCTATCTGTGCGAGCCAACAACACACAGGAGTATATCCTC 442

QY 117 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTirpThr 136
::: ::| |||||::|||::|||
Db 443 CTCGCATCCAAACACCTCCCACTATGACACATATTGCTTCAATGCCTCAGCTCCTCTTGAA 502

QY 137 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 156
||| ||| |||::: |||::: |||:::
Db 503 GAAGACTGT-----ACATCAGTCACAGACCTACCCAATTCCCTTCGATGGA 547

QY 157 ThrGlnThrThrGluPheIleValSerAspSerThr---TyrSerValAlaSerProTyr 175
||| ||| ::| ||| ||||| |||||
Db 548 CCAGTTACCATAACTATTGTCAACCGTGTGGCACCCGCTACAGCAAGAGGCGAGTAT 607

QY 176 SerThr-----IleProAlaProThr----- 182

Db 608 AGAACACACCAAGAGACATCGATGCCTCAAACATTATAGATGAGGATGTCACAGTGA 667

QY 183 -----ThrThrProProAla---ProAlaSerThrSerIleProArgArg 196
::: ||||| |||||
Db 668 TCCACCATTGAGAGAGACCCCAAGAGGCTACATTTTGCACACCGACCTTCCCACTTCA 727

QY 197 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThr---Glu 215
::: ::| ||| |||||::|||
Db 728 CAGCCTACTGGAGACCGGATGACGCCTTCTTTATTGGGAGCACCCCTGGCCACCATTGCA 787

QY 216 ThrGluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGly 235
||| |||::: ||| |||||
Db 788 ACTACTCCATGGGTTTCTGCCACACAAAAACAGAACCCAGGAACGGACCCAGTGGAAACCCG 847

QY 236 Val-----ProThrAlaLeuLeuValLeuAlaLeuLeuPhePheGlyAlaAlaAla 252
::: ||| |||||
Db 848 ATCCATTCAAACCCAGAGTACTACTTCAGACAACCCACAGGATGACTGATATAGACAGA 907

QY 253 GlyLeuGlyPheCysTyrValLysArgTyrValLys-----AlaPheProPheThrAsn 270
::: ::: ::: ||||| |||||
Db 908 AACAGCACCATGTCTCATGGAGAAAACCTGGACCCAGGAACCAACAGCCTCTTCAATAAC 967

QY 271 LysAsnGlnGlnLysGluMetIleGluThrLysValValLysGluGluLysAlaAsnAsp 290
||| ||| |||||
Db 968 CATGAGTATCAGGATGAAGAG---GAGACCCCAACATGTACAAGCACAAACCTGGGCAGAT 1024

QY 291 SerAsnProAsnGluGluSerLysLysThrAspLys-----AsnProGlu 305
||| ||| |||||

Search completed: August 17, 2004, 01:24:48
Job time : 101 secs

Db 1025 CCTAATAGCACAACAGAAAGCAGCTACCCAGAAGGAGAAGTGGTTTGAGAATGAATGG 1084

QY 306 GluSerLysSerPro 310
::: |||::|||

Db 1085 CAGGGGAAGAACCCA 1099

